

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 31, 2005, 00:22:11 ; Search time 1.43846 Seconds  
(without alignments)  
735.775 Million cell updates/sec

Title: US-10-049-822A-12

Perfect score: 58

Sequence: 1 YGRKKRRQRRR 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58	100.0	71	2	T09384
2	58	100.0	72	1	TN1JH4
3	58	100.0	86	1	TN1JZR
4	58	100.0	86	2	JC5591
5	58	100.0	86	2	A25700
6	58	100.0	86	2	S54381
7	58	100.0	86	2	S33982
8	58	100.0	87	2	T01665
9	58	100.0	95	1	TN1J12
10	58	100.0	101	1	E44001
11	58	100.0	101	2	T09446
12	55	94.8	86	1	TN1JND
13	46	79.3	100	1	TN1JSI
14	43	74.1	57	2	A34356
15	42	72.4	250	2	D38095
16	42	72.4	268	2	C38095
17	42	72.4	269	2	A38095
18	42	72.4	269	2	B38095
19	42	72.4	272	2	A38900
20	42	72.4	279	2	JH0402
21	42	72.4	303	2	JH0401
22	42	72.4	366	2	S61796
23	42	72.4	525	2	T48824
24	42	72.4	747	1	A57107
25	42	72.4	1193	2	A86193
26	41	70.7	37	2	S29829
27	41	70.7	47	2	F58208
28	41	70.7	47	2	E58208
29	41	70.7	58	2	S34045

30 41 70.7 294 2 E87538  
31 41 70.7 367 2 S59329  
32 41 70.7 417 2 E30341  
33 41 70.7 517 2 A45121  
34 41 70.7 770 2 G88445  
35 40 69.0 78 2 A40973  
36 40 69.0 79 2 S56116  
37 40 69.0 91 2 A59493  
38 40 69.0 118 2 S56117  
39 40 69.0 165 2 A59492  
40 40 69.0 371 2 B39625  
41 40 69.0 397 2 A39565  
42 40 69.0 399 2 A39625  
43 40 69.0 952 2 E86147  
44 39 67.2 46 2 A18865  
45 39 67.2 90 2 B32986

#### ALIGNMENTS

##### RESULT 1

T09384

trans-activating transcription regulator - human immunodeficiency virus type 1 (isolate  
C;Species: human immunodeficiency virus type 1, HIV-1  
C;Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004  
C;Accession: T09384

R;Michael, N.L.; Chang, G.; d'ARCY, L.A.; Ehrenberg, P.K.; Mariani, R.; Busch, M.P.; Bir

J; Virol. 69, 4228-4236, 1995

A;Title: Defective accessory genes in a human immunodeficiency virus type 1-infected lon

A;Reference number: Z16654; MUID:95287475; PMID:7769682

A;Accession: T09384

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-71 <MIC>

A;Cross-references: UNIPROT:Q71926; EMBL:U24451; NID:G829440; PIDN:AAA79576.1; PID:G8294

C;Genetics:

A;Gene: tat

C;Superfamily: AIDS trans-activating transcription regulator

C;Keywords: transcription

Query Match 100.0%; Score 58; DB 2; Length 71;  
Best Local Similarity 100.0%; Pred. No. 0.024;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 YGRKKRRQRRR 11

|||||

Db 47 YGRKKRRQRRR 57

##### RESULT 2

TN1JH4

trans-activating transcription regulator - human immunodeficiency virus type 1 (isolate  
C;Species: human immunodeficiency virus type 1, HIV-1  
C;Date: 30-Jun-1988 #sequence\_revision 30-Jun-1988 #text\_change 02-Jul-1998  
C;Accession: B25523

R;Desai, S.M.; Kalyanaraman, V.S.; Casey, J.M.; Srinivasan, A.; Andersen, P.R.; Devare,

Proc. Natl. Acad. Sci. U.S.A. 83, 8380-8384, 1986

A;Title: Molecular cloning and primary nucleotide sequence analysis of a distinct human

A;Reference number: A94136; MUID:87041461; PMID:3490666

A;Accession: B25523

A;Molecule type: DNA

A;Residues: 1-72 <DES>

A;Cross-references: GB:M13137; NID:G326460

A;Note: the GenBank entry A083AA PID:G209908 differs from the published sequence in tra

C;Genetics:

A;Gene: tat

C;Superfamily: AIDS trans-activating transcription regulator

C;Keywords: transcription regulation

Query Match 100.0%; Score 58; DB 1; Length 72;  
Best Local Similarity 100.0%; Pred. No. 0.024;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKKRQRRR 11  
|||||  
Db 47 YGRKKRQRRR 57

RESULT 3  
TNLJZR  
trans-activating transcription regulator - human immunodeficiency virus Zr-6  
C;Species: human immunodeficiency virus Zr-6  
C;Date: 30-Sep-1987 #sequence\_revision 30-Sep-1987 #text\_change 09-Jul-2004  
C;Accession: C26192  
R;Srinivasan, A.; Anand, R.; York, D.; Ranganathan, P.; Feorino, P.; Schochetman, G.; Cu  
Gene 52, 71-82, 1987  
A;Title: Molecular characterization of human immunodeficiency virus from Zaire: nucleoti  
A;Reference number: A26192; MUID:87248097; PMID:3036660  
A;Accession: C26192  
A;Molecule type: DNA  
A;Residues: 1-86 <SRI>  
C;Cross-references: UNIPROT:P04609; GB:K03458; GB:M16322; NID:G329398; PIDN:AAA45377.1;  
C;Genetics:  
A;Gene: tat  
A;Introns: 72/3  
C;Superfamily: AIDS trans-activating transcription regulator  
C;Keywords: AIDS; immunodeficiency; transcription regulation

Query Match 100.0%; Score 58; DB 1; Length 86;  
Best Local Similarity 100.0%; Pred. No. 0.028;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKKRQRRR 11  
|||||  
Db 47 YGRKKRQRRR 57

RESULT 4  
JC5591  
transactivator protein - human immunodeficiency virus type 1  
N;Alternate names: tat protein  
C;Species: human immunodeficiency virus type 1, HIV-1  
C;Date: 23-Sep-1997 #sequence\_revision 23-Sep-1997 #text\_change 17-Mar-1999  
C;Accession: JC5591  
R;Hoffmann, S.; Willbold, D.  
Biochem. Biophys. Res. Commun. 235, 806-811, 1997  
A;Title: A selection system to study protein-RNA interactions: Functional display of HIV  
A;Reference number: JC5591; MUID:97350867; PMID:9207243  
A;Accession: JC5591  
A;Molecule type: protein  
A;Residues: 1-86 <HO2>  
C;Comment: This protein is a key regulatory protein in the viral replication cycle and h  
C;Superfamily: AIDS trans-activating transcription regulator  
F;22-31/Region: cysteine-rich

Query Match 100.0%; Score 58; DB 2; Length 86;  
Best Local Similarity 100.0%; Pred. No. 0.028;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKKRQRRR 11  
|||||  
Db 47 YGRKKRQRRR 57

RESULT 5  
A25700  
trans-activating transcription regulator - human immunodeficiency virus type 1 (isolate  
C;Species: human immunodeficiency virus type 1, HIV-1  
C;Date: 28-Sep-1987 #sequence\_revision 28-Sep-1987 #text\_change 09-Jul-2004  
C;Accession: A25700  
R;Sodroski, J.; Patarca, R.; Rosen, C.; Wong-Staal, F.; Haseltine, W.  
Science 229, 74-77, 1985  
A;Reference number: A25700; MUID:85244627; PMID:2990041  
A;Accession: A25700  
A;Status: preliminary

A;Molecule type: mRNA  
A;Residues: 1-86 <SOD>  
A;Cross-references: UNIPROT:P04610  
C;Superfamily: AIDS trans-activating transcription regulator

Query Match 100.0%; Score 58; DB 2; Length 86;  
Best Local Similarity 100.0%; Pred. No. 0.028;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKKRQRRR 11  
|||||  
Db 47 YGRKKRQRRR 57

RESULT 6  
S54381  
tat protein - human immunodeficiency virus type 1  
C;Species: human immunodeficiency virus type 1, HIV-1  
C;Date: 15-Jul-1995 #sequence\_revision 01-Sep-1995 #text\_change 09-Jul-2004  
C;Accession: S54381  
R;Theodore, T.; Buckler-White, A.J.  
submitted to the EMBL Data Library, July 1989  
A;Reference number: S54377  
A;Accession: S54381  
A;Status: preliminary  
A;Molecule type: genomic RNA  
A;Residues: 1-86 <THE>  
A;Cross-references: UNIPROT:P12506; EMBL:M22639; NID:G329377; PIDN:AAA45363.1; PID:G3293  
C;Genetics: 72/2  
A;Introns:  
C;Superfamily: AIDS trans-activating transcription regulator

Query Match 100.0%; Score 58; DB 2; Length 86;  
Best Local Similarity 100.0%; Pred. No. 0.028;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKKRQRRR 11  
|||||  
Db 47 YGRKKRQRRR 57

RESULT 7  
S33982  
trans-activating transcription regulator - human immunodeficiency virus type 1  
C;Species: human immunodeficiency virus type 1, HIV-1  
C;Date: 06-Oct-1994 #sequence\_revision 23-Feb-1996 #text\_change 09-Jul-2004  
C;Accession: S33982; S19864  
R;Carlini, F.  
submitted to the EMBL Data Library, November 1991  
A;Reference number: S33979  
A;Accession: S33982  
A;Molecule type: DNA  
A;Residues: 1-86 <CAR>  
A;Cross-references: UNIPROT:P04606; EMBL:Z11530; NID:G60192; PIDN:CAA77625.1; PID:G60196  
R;Siderovski, D.P.; Matsuyama, T.; Frigerio, E.; Chui, S.; Min, X.; Erfle, H.; Summer-Sm  
Nucleic Acids Res. 20, 5311-5320, 1992  
A;Title: Random mutagenesis of the human immunodeficiency virus type-1 trans-activator  
A;Reference number: S26385; MUID:93065196; PMID:1437550  
A;Accession: S26385  
A;Molecule type: nucleic acid  
A;Residues: 1-86 <SID>  
A;Cross-references: EMBL:X64650; NID:G60144; PIDN:CAA45921.1; PID:G60145  
C;Genetics:  
A;Gene: tat  
A;Introns: 72/2  
C;Superfamily: AIDS trans-activating transcription regulator  
C;Keywords: AIDS; immunodeficiency

Query Match 100.0%; Score 58; DB 2; Length 86;  
Best Local Similarity 100.0%; Pred. No. 0.028;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKKRQRRR 11

Db 1 YGRKKRQRRR 57  
|||||  
RESULT 8  
T01665  
tat protein - human immunodeficiency virus type 1  
C;Species: human immunodeficiency virus type 1, HIV-1  
C;Date: 19-Feb-1999 #sequence\_revision 19-Feb-1999 #text\_change 09-Jul-2004  
C;Accession: T01665  
R;Alizon, M.; Wain-Hobson, S.; Gluckman, J.C.; Sonigo, P.  
Cell 46, 63-74, 1986  
A;Title: Genetic variability of the AIDS virus: Nucleotide sequence analysis of two isolates  
A;Reference number: Z14389; MUID: 86245056; PMID: 2424612  
A;Accession: T01665  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-87 <ALI>  
A;Cross-references: UNIPROT:P04613; EMBL:K03456; NID:G60228; PIDN:CAA28015.1; PID:G60233  
C;Genetics:  
A;Introns: 72/2  
C;Superfamily: AIDS trans-activating transcription regulator  
Query Match 100.0%; Score 58; DB 2; Length 87;  
Best Local Similarity 100.0%; Pred. No. 0.028;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 YGRKKRQRRR 11  
|||||  
Db 47 YGRKKRQRRR 57  
RESULT 9  
TNLJ12  
trans-activating transcription regulator - human immunodeficiency virus type 1 (isolate  
C;Species: human immunodeficiency virus type 1, HIV-1  
A;Note: host Homo sapiens (man)  
C;Date: 04-Dec-1986 #sequence\_revision 04-Dec-1986 #text\_change 09-Jul-2004  
C;Accession: A04017  
R;Arya, S.K.; Gallo, R.C.  
Proc. Natl. Acad. Sci. U.S.A. 83, 2209-2213, 1986  
A;Title: Three novel genes of human T-lymphotropic virus type III: immune reactivity of  
A;Reference number: A94093; MUID: 86177573; PMID: 3008154  
A;Accession: A04017  
A;Molecule type: DNA  
A;Residues: 1-95 <ARY>  
A;Cross-references: UNIPROT:P04326  
C;Genetics:  
A;Gene: tat  
C;Superfamily: AIDS trans-activating transcription regulator  
Query Match 100.0%; Score 58; DB 1; Length 95;  
Best Local Similarity 100.0%; Pred. No. 0.03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 YGRKKRQRRR 11  
|||||  
Db 56 YGRKKRQRRR 66  
RESULT 10  
E44001  
trans-activating transcription regulator - human immunodeficiency virus type 1 (strain x  
N;Alternate names: tat protein  
C;Species: human immunodeficiency virus type 1, HIV-1  
A;Note: host Homo sapiens (man)  
C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 09-Jul-2004  
C;Accession: E44001  
R;Li, Y.; Hui, H.; Burgess, C.J.; Price, R.W.; Sharp, P.M.; Hahn, B.H.; Shaw, G.M.  
J. Virol. 66, 6587-6600, 1992  
A;Title: Complete nucleotide sequence, genome organization, and biological properties of  
A;Reference number: A44001; MUID: 93021387; PMID: 1404605

A;Accession: E44001  
A;Molecule type: DNA  
A;Residues: 1-101 <LIY>  
A;Cross-references: UNIPROT:P35965; GB:M93258  
C;Genetics:  
A;Gene: tat  
A;Introns: 72/2  
C;Superfamily: AIDS trans-activating transcription regulator  
C;Keywords: AIDS; immunodeficiency; transcription regulation  
Query Match 100.0%; Score 58; DB 1; Length 101;  
Best Local Similarity 100.0%; Pred. No. 0.032;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 YGRKKRQRRR 11  
|||||  
Db 47 YGRKKRQRRR 57  
RESULT 11  
T09446  
tat protein - human immunodeficiency virus type 1 (strain JRFL)  
C;Species: human immunodeficiency virus type 1, HIV-1  
C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 09-Jul-2004  
C;Accession: T09446  
R;Pang, S.; Vinters, H.V.; Akashi, T.; O'Brien, W.A.; Chen, I.S.; Koyanagi, Y.; Namazie,  
submitted to the EMBL Data Library, July 1996  
A;Reference number: Z16673  
A;Accession: T09446  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-101 <PAN>  
A;Cross-references: UNIPROT:Q75758; EMBL:U63632; NID:G1465777; PID:G1465783  
C;Genetics:  
A;Gene: tat  
A;Introns: 72/2  
C;Superfamily: AIDS trans-activating transcription regulator  
Query Match 100.0%; Score 58; DB 2; Length 101;  
Best Local Similarity 100.0%; Pred. No. 0.032;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 YGRKKRQRRR 11  
|||||  
Db 47 YGRKKRQRRR 57  
RESULT 12  
TNLJND  
trans-activating transcription regulator - human immunodeficiency virus type 1 (isolate  
C;Species: human immunodeficiency virus type 1, HIV-1  
A;Note: host Homo sapiens (man)  
C;Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 09-Jul-2004  
C;Accession: JQ0071  
R;Spire, B.; Sire, J.; Zachar, V.; Rey, F.; Barre-Sinoussi, F.; Galibert, F.; Hampe, A.;  
Gene 81, 275-284, 1989  
A;Title: Nucleotide sequence of HIV1-NDK: a highly cytopathic strain of the human immuno  
A;Reference number: JQ0065; MUID: 90034200; PMID: 2806917  
A;Accession: JQ0071  
A;Molecule type: DNA  
A;Residues: 1-86 <SPI>  
A;Cross-references: UNIPROT:P18804; GB:M27323; NID:G328154; PIDN:AAA44866.1; PID:G328155  
C;Genetics:  
A;Gene: tat  
C;Superfamily: AIDS trans-activating transcription regulator  
C;Keywords: AIDS; immunodeficiency; transcription  
Query Match 94.8%; Score 55; DB 1; Length 86;  
Best Local Similarity 90.9%; Pred. No. 0.079;  
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 YGRKKRQRRR 11  
|||||

Db 47 YGRKKRQRRK 57

## RESULT 13

TNLUSI

trans-activating transcription regulator - simian immunodeficiency virus SIVcpz

C;Species: simian immunodeficiency virus SIVcpz

A;Note: host Pan troglodytes (chimpanzee)

C;Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 09-Jul-2004

C;Accession: S09987

R;Huet, T.; Cheymier, R.; Meyerhans, A.; Roelants, G.; Wain-Hobson, S.

Nature 345, 356-359, 1990

A;Title: Genetic organization of a chimpanzee lentivirus related to HIV-1.

A;Reference number: S09983; MUID:90259077; PMID:2188136

A;Accession: S09987

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-100 &lt;HUE&gt;

A;Cross-references: UNIPROT:P17285; EMBL:X52154; NID:g58866; PIDN:CAA36404.1; PID:g76308

C;Genetics:

A;Gene: tat

A;Introns: 73/2

C;Superfamily: AIDS trans-activating transcription regulator

C;Keywords: AIDS; immunodeficiency; transcription

Query Match	79.3%	Score 46;	DB 1;	Length 100;
Best Local Similarity	81.8%	Fred. No. 2.1;		
Matches	9;	Conservative 0;	Mismatches 2;	Indels 0; Gaps 0;

Qy 1 YGRKKRQRRR 11

Db 47 YGRKKRTTTR 57

## RESULT 14

A34356

protamine - Japanese quail

C;Species: Coturnix coturnix japonica (Japanese quail)

C;Date: 15-Jun-1990 #sequence\_revision 15-Jun-1990 #text\_change 09-Jul-2004

C;Accession: A34356

R;Oliva, R.; Goren, R.; Dixon, G.H.

J. Biol. Chem. 264, 17627-17630, 1989

A;Title: Quail (Coturnix japonica) protamine, full-length cDNA sequence, and the function

A;Reference number: A34356; MUID:90036816; PMID:2808336

A;Accession: A34356

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-57 &lt;OLI&gt;

A;Cross-references: UNIPROT:P14402; GB:M30275; NID:g213612; PIDN:AAA49498.1; PID:g213613

C;Superfamily: sperm histone

C;Keywords: DNA binding; nucleus; phosphoprotein

Query Match	74.1%	Score 43;	DB 2;	Length 57;
Best Local Similarity	70.0%	Fred. No. 3.9;		
Matches	7;	Conservative 3;	Mismatches 0;	Indels 0; Gaps 0;

Qy 1 YGRKKRQRRR 10

Db 47 YGRRRRRRRR 56

## RESULT 15

D38095

T-cell-specific transcription factor 1 splice form D - human

N;Alternate names: transcription factor TCF-1D

C;Species: Homo sapiens (man)

C;Date: 19-May-1994 #sequence\_revision 19-May-1994 #text\_change 16-Aug-2004

C;Accession: D38095; S61877; S61800

R;van de Wetering, M.; Oosterwegel, M.; Holstege, F.; Dooyes, D.; Suijkerbuijk, R.; Geuz

J. Biol. Chem. 267, 8530-8536, 1992

A;Title: The human T cell transcription factor-1 gene. Structure, localization, and prom

A;Reference number: A38095; MUID:92235082; PMID:1569101

A;Accession: D38095

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-250 &lt;VAN&gt;

A;Cross-references: GB:X63901

R;Mayer, K.; Wolff, E.; Clevers, H.; Ballhausen, W.G.

submitted to the EMBL Data Library, January 1995

A;Description: The human high mobility group (HMG)-box transcription factor TCF-1: novel

A;Reference number: S61877

A;Accession: S61877

A;Molecule type: mRNA

A;Residues: 1-250 &lt;WAY&gt;

A;Cross-references: EMBL:Z47361; NID:g619881; PIDN:CAA87439.1; PID:g619882

R;Mayer, K.; Wolff, E.; Clevers, H.; Ballhausen, W.G.

Biochim. Biophys. Acta 1263, 169-172, 1995

A;Title: The human high mobility group (HMG)-box transcription factor TCF-1: novel isofo

A;Reference number: S61796; MUID:95367594; PMID:7640309

A;Accession: S61800

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 244-250 &lt;MAW&gt;

A;Cross-references: EMBL:Z47361

C;Genetics:

A;Introns: 32/3; 68/1; 97/2; 137/2; 191/3; 227/3; 243/3

C;Superfamily: HMG box homology

C;Keywords: alternative splicing; DNA binding; transcription factor

P;151-226/domain: HMG box homology &lt;HMG1&gt;

Query Match	72.4%	Score 42;	DB 2;	Length 250;
Best Local Similarity	63.6%	Fred. No. 18;		
Matches	7;	Conservative 2;	Mismatches 2;	Indels 0; Gaps 0;

Qy 1 YGRKKRQRRR 11

Db 227 YGRKKRRRREK 237

Search completed: March 31, 2005, 00:31:36

Job time : 3.43846 secs



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OM protein - protein search, using sw model

Run on: March 31, 2005, 00:19:36 ; Search time 6.13461 Seconds  
(without alignments)  
918.211 Million cell updates/sec

Title: US-10-049-822A-12  
Perfect score: 58  
Sequence: 1 YGRKKRQRRR 11

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58	100.0	58	1 TAT_HV1B5	P04612 human immun
2	58	100.0	64	2 Q6QAV2	Q6QAV2 human immun
3	58	100.0	65	2 Q75540	Q75540 human immun
4	58	100.0	65	2 Q75544	Q75544 human immun
5	58	100.0	68	2 Q6QAV4	Q6QAV4 human immun
6	58	100.0	70	2 Q6MQ1	Q6MQ1 human immun
7	58	100.0	71	2 Q40224	Q40224 human immun
8	58	100.0	71	2 Q40225	Q40225 human immun
9	58	100.0	71	2 Q40226	Q40226 human immun
10	58	100.0	71	2 Q40227	Q40227 human immun
11	58	100.0	71	2 Q40228	Q40228 human immun
12	58	100.0	71	2 Q40231	Q40231 human immun
13	58	100.0	71	2 Q40232	Q40232 human immun
14	58	100.0	71	2 Q40233	Q40233 human immun
15	58	100.0	71	2 Q40234	Q40234 human immun
16	58	100.0	71	2 Q8QDX8	Q8QDX8 human immun
17	58	100.0	71	2 Q8QDX2	Q8QDX2 human immun
18	58	100.0	71	2 Q6MP3	Q6MP3 human immun
19	58	100.0	71	2 Q6MP6	Q6MP6 human immun
20	58	100.0	71	2 Q6MP9	Q6MP9 human immun
21	58	100.0	71	2 Q6MQ3	Q6MQ3 human immun
22	58	100.0	71	2 Q6MQ5	Q6MQ5 human immun
23	58	100.0	71	2 Q6MQ7	Q6MQ7 human immun
24	58	100.0	71	2 Q6MQ9	Q6MQ9 human immun
25	58	100.0	71	2 Q6MR1	Q6MR1 human immun
26	58	100.0	71	2 Q6MR5	Q6MR5 human immun
27	58	100.0	71	2 Q6MR7	Q6MR7 human immun
28	58	100.0	71	2 Q6MR9	Q6MR9 human immun
29	58	100.0	71	2 Q6MS1	Q6MS1 human immun
30	58	100.0	71	2 Q6MS3	Q6MS3 human immun
31	58	100.0	71	2 Q6MS5	Q6MS5 human immun

32	58	100.0	71	2	Q6MS7	Q6MS7 human immun
33	58	100.0	71	2	Q6MS9	Q6MS9 human immun
34	58	100.0	71	2	Q6MT1	Q6MT1 human immun
35	58	100.0	71	2	Q71875	Q71875 human immun
36	58	100.0	71	2	Q71886	Q71886 human immun
37	58	100.0	71	2	Q71891	Q71891 human immun
38	58	100.0	71	2	Q71898	Q71898 human immun
39	58	100.0	71	2	Q71905	Q71905 human immun
40	58	100.0	71	2	Q71912	Q71912 human immun
41	58	100.0	71	2	Q71919	Q71919 human immun
42	58	100.0	71	2	Q71926	Q71926 human immun
43	58	100.0	71	2	Q71932	Q71932 human immun
44	58	100.0	71	2	Q71939	Q71939 human immun
45	58	100.0	71	2	Q71945	Q71945 human immun

#### ALIGNMENTS

RESULT:1

TAT\_HV1B5

ID TAT HV1B5 STANDARD; PRT; 58 AA.

AC P04612;

DT 13-AUG-1987 (Rel. 05, Created)

DT 13-AUG-1987 (Rel. 05, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE TAT protein (Transactivating regulatory protein) (Fragment) .

GN Name=TAT;

OS Human immunodeficiency virus type 1 (BH5 isolate) (HIV-1).

OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.

OK NCBI\_TaxID=11682;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=85111123; PubMed=2578615;

RA Ratner L., Haseltine W.A., Patarca R., Livak K.J., Starcich B.R.,

RA Josephs S.F., Doran E.R., Rafalski J.A., Whitehorn E.A.,

RA Baumerster K., Ivanoff L., Petteway S.R. Jr., Pearson M.B.,

RA Lautenberger J.A., Papas T.S., Grayeb J., Chang N.T., Gallo R.C.,

RA Wong-Staal F.;

RT "Complete nucleotide sequence of the AIDS virus, HTLV-III.";

RL Nature 313:277-284(1985)

CC -!- FUNCTION: Transcriptional regulator that acts by binding to the

CC trans-activating responsive sequence (TAR) RNA element and

CC activates transcription initiation and/or elongation from the LTR

CC promoter.

CC -!- SUBUNIT: Binds cyclin T1 (By similarity).

CC -!- SUBCELLULAR LOCATION: Nuclear; nucleolar.

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CC EMBL; K02012; AAA44656.1; --

CC HSSP; P04610; 1JFW.

CC HIV; K02012; TAT\$BH5.

CC InterPro; IPR001831; IV\_Tat.

CC Pfam; PF00539; Tat; 1.

CC PRINTS; PR00055; HIVTATDOMAIN.

CC Activator; AIDS; Nuclear protein; RNA-binding;

CC Transcription regulation.

KW NON TER 58 58

FT SEQUENCE 58 AA; 6800 MW; E36C21F8F8D813E3 CRC64;

Query Match 100.0%; Score 58; DB 1; Length 58;

Best local similarity 100.0%; Pred. No. 0.015;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRKKRQRRR 11

|||||||

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Db          47 YGRKKRQRRR 57

RESULT 2
Q6QAV2      PRELIMINARY;      PRT;      64 AA.
AC Q6QAV2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Tat protein (Fragment).
GN Name=tat;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Lorenzo E., Herrera R.J., Lai S., Fischl M.A., Hill M.D.;
RA Andreo S.M.S., Barra L.A.C., Costa L.J., Sucupira M.C.A.,
RA Souza I.E.L., Diaz R.S.;
RT "HIV Type 1 Transmission by Human Bite.";
RL AIDS Res. Hum. Retroviruses 20:349-350(2004).
CC -1- FUNCTION: Transcriptional regulator that acts by binding to the
CC trans-activating responsive sequence (TAR) RNA element and
CC activates transcription initiation and/or elongation from the LTR
CC promoter (By similarity).
DR EMBL: AY549944; AAS67918.1; -.
DR GO: GO:0042025; C:host cell nucleus; IEA.
DR GO: GO:0005634; C:nucleus; IEA.
DR GO: GO:0003723; F:RNA binding; IEA.
DR GO: GO:0003700; F:transcription factor activity; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR001831, IV_Tat.
DR Pfam: PF00539; Tat; 1.
DR PRINTS: PR00055; HIVTATDOMAIN.
DR Activator; Nuclear protein; RNA-binding; Transcription;
KW Transcription regulation.
FT NON TER 1
SQ SEQUENCE 64 AA; 7474 MW; E13926D6C42D72D3 CRC64;

Query Match 100.0%; Score 58; DB 2; Length 64;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKKRQRRR 11
| | | | | | | |
Db 39 YGRKKRQRRR 49

RESULT 3
Q75540      PRELIMINARY;      PRT;      65 AA.
AC Q75540;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Tat protein (Fragment).
GN Name=tat;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Lorenzo E., Herrera R.J., Lai S., Fischl M.A., Hill M.D.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Transcriptional regulator that acts by binding to the
CC trans-activating responsive sequence (TAR) RNA element and
CC activates transcription initiation and/or elongation from the LTR
CC promoter (By similarity).
DR EMBL: U57248; AAB17808.1; -.
DR HSSP: P12506; ITEC.
DR GO: GO:0042025; C:host cell nucleus; IEA.
DR GO: GO:0005634; C:nucleus; IEA.
DR GO: GO:0003723; F:RNA binding; IEA.
DR InterPro: IPR001831, IV_Tat.
DR Pfam: PF00539; Tat; 1.
DR PRINTS: PR00055; HIVTATDOMAIN.
DR Activator; Nuclear protein; RNA-binding; Transcription;
KW Transcription regulation.
FT NON TER 1
SQ SEQUENCE 64 AA; 7474 MW; E13926D6C42D72D3 CRC64;

Query Match 100.0%; Score 58; DB 2; Length 64;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKKRQRRR 11
| | | | | | | |
Db 39 YGRKKRQRRR 49

RESULT 4
Q75544      PRELIMINARY;      PRT;      65 AA.
AC Q75544;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Tat protein (Fragment).
GN Name=tat;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Lorenzo E., Herrera R.J., Lai S., Fischl M.A., Hill M.D.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Transcriptional regulator that acts by binding to the
CC trans-activating responsive sequence (TAR) RNA element and
CC activates transcription initiation and/or elongation from the LTR
CC promoter (By similarity).
DR EMBL: U57252; AAB17812.1; -.
DR HSSP: P12506; ITEC.
DR GO: GO:0042025; C:host cell nucleus; IEA.
DR GO: GO:0005634; C:nucleus; IEA.
DR GO: GO:0003723; F:RNA binding; IEA.
DR GO: GO:0003700; F:transcription factor activity; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR001831, IV_Tat.
DR Pfam: PF00539; Tat; 1.
DR Activator; Nuclear protein; RNA-binding; Transcription;
KW Transcription regulation.
FT NON TER 1
SQ SEQUENCE 65 AA; 7677 MW; 91584F861F6A8362 CRC64;

Query Match 100.0%; Score 58; DB 2; Length 65;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKKRQRRR 11
| | | | | | | |
Db 47 YGRKKRQRRR 57

RESULT 5
Q6QAV4      PRELIMINARY;      PRT;      68 AA.
AC Q6QAV4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Tat protein (Fragment).
GN Name=tat;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

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DR GO: GO:0003700; F:transcription factor activity; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR001831, IV_Tat.
DR Pfam: PF00539; Tat; 1.
DR PRINTS: PR00055; HIVTATDOMAIN.
DR Activator; Nuclear protein; RNA-binding; Transcription;
KW Transcription regulation.
FT NON TER 1
SQ SEQUENCE 65 AA; 7619 MW; 91584F861A2F9736 CRC64;

Query Match 100.0%; Score 58; DB 2; Length 65;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKKRQRRR 11
| | | | | | | |
Db 47 YGRKKRQRRR 57

RESULT 4
Q75544      PRELIMINARY;      PRT;      65 AA.
AC Q75544;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Tat protein (Fragment).
GN Name=tat;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Lorenzo E., Herrera R.J., Lai S., Fischl M.A., Hill M.D.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Transcriptional regulator that acts by binding to the
CC trans-activating responsive sequence (TAR) RNA element and
CC activates transcription initiation and/or elongation from the LTR
CC promoter (By similarity).
DR EMBL: U57252; AAB17812.1; -.
DR HSSP: P12506; ITEC.
DR GO: GO:0042025; C:host cell nucleus; IEA.
DR GO: GO:0005634; C:nucleus; IEA.
DR GO: GO:0003723; F:RNA binding; IEA.
DR GO: GO:0003700; F:transcription factor activity; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR001831, IV_Tat.
DR Pfam: PF00539; Tat; 1.
DR Activator; Nuclear protein; RNA-binding; Transcription;
KW Transcription regulation.
FT NON TER 1
SQ SEQUENCE 65 AA; 7677 MW; 91584F861F6A8362 CRC64;

Query Match 100.0%; Score 58; DB 2; Length 65;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKKRQRRR 11
| | | | | | | |
Db 47 YGRKKRQRRR 57

RESULT 5
Q6QAV4      PRELIMINARY;      PRT;      68 AA.
AC Q6QAV4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Tat protein (Fragment).
GN Name=tat;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

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OX NCBI_TaxID=11676;
RN SEQUENCE FROM N.A.
RP Andre S.M.S., Barra L.A.C., Costa L.J., Sucupira M.C.A.,
RA Souza I.E.L., Diaz R.S.;
RT "HIV Type 1 Transmission by Human Bite.";
RL AIDS Res. Hum. Retroviruses 20:349-350(2004).
CC -1- FUNCTION: Transcriptional regulator that acts by binding to the
CC trans-activating responsive sequence (TAR) RNA element and
CC activates transcription initiation and/or elongation from the LTR
CC promoter (By similarity).
DR EMBL: AY549942; AAS67916.1; -.
DR GO: GO:0042025; C:host cell nucleus; IEA.
DR GO: GO:0005634; C:nucleus; IEA.
DR GO: GO:0003723; F:RNA binding; IEA.
DR GO: GO:0003700; F:transcription factor activity; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR001831, IV_Tat.
DR Pfam: PF00539; Tat; 1.
DR PRINTS: PR00055; HIVTATDOMAIN.
DR Activator; Nuclear protein; RNA-binding; Transcription;
KW Transcription regulation.
FT NON TER 1
SQ SEQUENCE 68 AA; 7983 MW; 326A05D50078CD29 CRC64;

Query Match 100.0%; Score 58; DB 2; Length 68;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKKRQRRR 11
Db |||||
43 YGRKKRQRRR 53

RESULT 6
Q66MQ1 PRELIMINARY; PRT; 70 AA.
AC Q66MQ1 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Tat protein (Fragment).
GN Name=tat;
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN SEQUENCE FROM N.A.
RP Herring B.L., Grant R.M., Delwart E.L.;
RT "No superinfection among seroconcordant couples after well-defined
RL exposure.";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Transcriptional regulator that acts by binding to the
CC trans-activating responsive sequence (TAR) RNA element and
CC activates transcription initiation and/or elongation from the LTR
CC promoter (By similarity).
DR EMBL: AY686119; AAU05440.1; -.
DR InterPro: IPR001831, IV_Tat.
DR Pfam: PF00539; Tat; 1.
DR PRINTS: PR00055; HIVTATDOMAIN.
DR Activator; Nuclear protein; RNA-binding; Transcription;
KW Transcription regulation.
FT NON TER 70
SQ SEQUENCE 70 AA; 8096 MW; 28E39B5672863DBB CRC64;

Query Match 100.0%; Score 58; DB 2; Length 70;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKKRQRRR 11
Db |||||
47 YGRKKRQRRR 57
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RESULT 7
O40224 PRELIMINARY; PRT; 71 AA.
ID O40224 (TrEMBLrel. 05, Created)
AC O40224 (TrEMBLrel. 05, Last sequence update)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-JAN-1998 (TrEMBLrel. 05, Last annotation update)
DE Tat protein (Fragment).
GN Name=tat;
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN SEQUENCE FROM N.A.
RP STRAIN=AD93-A3tat;
RC MEDLINE=97335179; PubMed=9191845; DOI=10.1006/viro.1997.8586;
RA Kirchhoff F., Greenough T.C., Hamacher M., Sullivan J.L.,
RA Desrosiers R.C.;
RT "Activity of human immunodeficiency virus type 1 promoter/TAR regions
RT and tat1 genes derived from individuals with different rates of
RT disease progression.";
RL Virology 232:319-331(1997).
CC -1- FUNCTION: Transcriptional regulator that acts by binding to the
CC trans-activating responsive sequence (TAR) RNA element and
CC activates transcription initiation and/or elongation from the LTR
CC promoter (By similarity).
DR EMBL: AF000522; AAB62521.1; -.
DR HSP; P04610; 1JFW.
DR GO: GO:0042025; C:host cell nucleus; IEA.
DR GO: GO:0005634; C:nucleus; IEA.
DR GO: GO:0003723; F:RNA binding; IEA.
DR GO: GO:0003700; F:transcription factor activity; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR001831, IV_Tat.
DR Pfam: PF00539; Tat; 1.
DR Activator; Nuclear protein; RNA-binding; Transcription;
KW Transcription regulation.
FT NON TER 71
SQ SEQUENCE 71 AA; 8211 MW; B3031C7AF5EF30E0 CRC64;

Query Match 100.0%; Score 58; DB 2; Length 71;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKKRQRRR 11
Db |||||
47 YGRKKRQRRR 57

RESULT 8
O40225 PRELIMINARY; PRT; 71 AA.
ID O40225 (TrEMBLrel. 05, Created)
AC O40225 (TrEMBLrel. 05, Last sequence update)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-JAN-1998 (TrEMBLrel. 05, Last annotation update)
DE Tat protein (Fragment).
GN Name=tat;
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN SEQUENCE FROM N.A.
RP STRAIN=BJ93-A3tat;
RC MEDLINE=97335179; PubMed=9191845; DOI=10.1006/viro.1997.8586;
RA Kirchhoff F., Greenough T.C., Hamacher M., Sullivan J.L.,
RA Desrosiers R.C.;
RT "Activity of human immunodeficiency virus type 1 promoter/TAR regions
RT and tat1 genes derived from individuals with different rates of
RT disease progression.";
RL Virology 232:319-331(1997).
CC -1- FUNCTION: Transcriptional regulator that acts by binding to the
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CC trans-activating responsive sequence (TAR) RNA element and
CC activates transcription initiation and/or elongation from the LTR
CC promoter (By similarity).
DR EMBL; AF000523; AAB62522.1; -.
DR HSSP; P12506; ITBC.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001831; IV_Tat.
DR Pfam; PF00539; Tat; 1.
DR PRINTS; PR00055; HIVTATDOMAIN.
KW Activator; Nuclear protein; RNA-binding; Transcription;
KW Transcription regulation.
FT NON_TER 71
SQ SEQUENCE 71 AA; 8179 MW; CE411588EB96209F CRC64;

Query Match 100.0%; Score 58; DB 2; Length 71;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKKRQRRR 11
Dd |||||
47 YGRKKRQRRR 57

RESULT 9
O40226 PRELIMINARY; PRT; 71 AA.
AC O40226;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Tat protein (Fragment).
GN Name=tat;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BT94-A2tat;
RX MEDLINE=97335179; PubMed=9191845; DOI=10.1006/viro.1997.8586;
RA Kirchhoff F., Greenough T.C., Hamacher M., Sullivan J.L.,
RA Desrosiers R.C.;
RT "Activity of human immunodeficiency virus type 1 promoter/TAR regions
RT and tat1 genes derived from individuals with different rates of
RT disease progression.";
RL Virology 232:319-331(1997).
CC -!- FUNCTION: Transcriptional regulator that acts by binding to the
CC trans-activating responsive sequence (TAR) RNA element and
CC activates transcription initiation and/or elongation from the LTR
CC promoter (By similarity).
DR EMBL; AF000525; AAB62524.1; -.
DR HSSP; P04610; IJFW.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001831; IV_Tat.
DR Pfam; PF00539; Tat; 1.
DR PRINTS; PR00055; HIVTATDOMAIN.
KW Activator; Nuclear protein; RNA-binding; Transcription;
KW Transcription regulation.
FT NON_TER 71
SQ SEQUENCE 71 AA; 8247 MW; C880BD85C90230E5 CRC64;

Query Match 100.0%; Score 58; DB 2; Length 71;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKKRQRRR 11
Dd |||||
47 YGRKKRQRRR 57

RESULT 11
O40228 PRELIMINARY; PRT; 71 AA.
AC O40228;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Tat protein (Fragment).
GN Name=tat;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DJ93-A1tat;
RX MEDLINE=97335179; PubMed=9191845; DOI=10.1006/viro.1997.8586;
RA Kirchhoff F., Greenough T.C., Hamacher M., Sullivan J.L.,
RA Desrosiers R.C.;
RT "Activity of human immunodeficiency virus type 1 promoter/TAR regions
RT and tat1 genes derived from individuals with different rates of
RT disease progression.";
RL Virology 232:319-331(1997).
CC -!- FUNCTION: Transcriptional regulator that acts by binding to the
CC trans-activating responsive sequence (TAR) RNA element and
CC activates transcription initiation and/or elongation from the LTR
CC promoter (By similarity).
DR EMBL; AF000524; AAB62523.1; -.
DR HSSP; P04610; IJFW.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001831; IV_Tat.
DR Pfam; PF00539; Tat; 1.
DR PRINTS; PR00055; HIVTATDOMAIN.
KW Activator; Nuclear protein; RNA-binding; Transcription;
KW Transcription regulation.
FT NON_TER 71
SQ SEQUENCE 71 AA; 8337 MW; 50B96328495E6A2C CRC64;

Query Match 100.0%; Score 58; DB 2; Length 71;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKKRQRRR 11

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Db |||||
47 YGRKKRQRRR 57

RESULT 10
O40227 PRELIMINARY; PRT; 71 AA.
AC O40227;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Tat protein (Fragment).
GN Name=tat;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CH94-A2tat;
RX MEDLINE=97335179; PubMed=9191845; DOI=10.1006/viro.1997.8586;
RA Kirchhoff F., Greenough T.C., Hamacher M., Sullivan J.L.,
RA Desrosiers R.C.;
RT "Activity of human immunodeficiency virus type 1 promoter/TAR regions
RT and tat1 genes derived from individuals with different rates of
RT disease progression.";
RL Virology 232:319-331(1997).
CC -!- FUNCTION: Transcriptional regulator that acts by binding to the
CC trans-activating responsive sequence (TAR) RNA element and
CC activates transcription initiation and/or elongation from the LTR
CC promoter (By similarity).
DR EMBL; AF000525; AAB62524.1; -.
DR HSSP; P04610; IJFW.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001831; IV_Tat.
DR Pfam; PF00539; Tat; 1.
DR PRINTS; PR00055; HIVTATDOMAIN.
KW Activator; Nuclear protein; RNA-binding; Transcription;
KW Transcription regulation.
FT NON_TER 71
SQ SEQUENCE 71 AA; 8247 MW; C880BD85C90230E5 CRC64;

Query Match 100.0%; Score 58; DB 2; Length 71;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKKRQRRR 11
Dd |||||
47 YGRKKRQRRR 57

RESULT 11
O40228 PRELIMINARY; PRT; 71 AA.
AC O40228;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Tat protein (Fragment).
GN Name=tat;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DJ93-A1tat;
RX MEDLINE=97335179; PubMed=9191845; DOI=10.1006/viro.1997.8586;
RA Kirchhoff F., Greenough T.C., Hamacher M., Sullivan J.L.,
RA Desrosiers R.C.;
RT "Activity of human immunodeficiency virus type 1 promoter/TAR regions

```

RT and tat1 genes derived from individuals with different rates of  
 RT disease progression.";  
 RL Virology 232:319-331(1997).  
 CC -1- FUNCTION: Transcriptional regulator that acts by binding to the  
 CC trans-activating responsive sequence (TAR) RNA element and  
 CC activates transcription initiation and/or elongation from the LTR  
 CC promoter (By similarity).  
 DR EMEL; AF000526; AAB62525.1; -.  
 DR HSP; P04610; IJFW.  
 DR GO: GO:0042025; C:host cell nucleus; IEA.  
 DR GO: GO:0005634; C:nucleus; IEA.  
 DR GO: GO:0003723; F:RNA binding; IEA.  
 DR GO: GO:0003700; F:transcription factor activity; IEA.  
 DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro; IPR001831; IV\_Tat.  
 DR Pfam; PF00539; Tat; 1.  
 DR PRINTS; PR00055; HIVTATDOMAIN.  
 KW Activator; Nuclear protein; RNA-binding; Transcription;  
 KW Transcription regulation.  
 FT NON TER 71  
 SQ SEQUENCE 71 AA; 8191 MW; C880A34AEAFF30E5 CRC64;  
 Query Match 100.0%; Score 58; DB 2; Length 71;  
 Best Local Similarity 100.0%; Pred. No. 0.018;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YGRKKRRQRRR 11  
 DB 47 YGRKKRRQRRR 57  
 RESULT 12  
 O40231 PRELIMINARY; PRT; 71 AA.  
 ID O40231  
 AC O40231  
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Tat protein (Fragment).  
 GN Name=tat;  
 OS Human immunodeficiency virus 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=HP91-Altat;  
 RX MEDLINE=97335179; PubMed=9191845; DOI=10.1006/viro.1997.8586;  
 RA Kirchhoff F., Greenough T.C., Hamacher M., Sullivan J.L.,  
 RA Desrosiers R.C.;  
 RT "Activity of human immunodeficiency virus type 1 promoter/TAR regions  
 RT and tat1 genes derived from individuals with different rates of  
 RT disease progression.";  
 RL Virology 232:319-331(1997).  
 CC -1- FUNCTION: Transcriptional regulator that acts by binding to the  
 CC trans-activating responsive sequence (TAR) RNA element and  
 CC activates transcription initiation and/or elongation from the LTR  
 CC promoter (By similarity).  
 DR EMEL; AF000530; AAB62529.1; -.  
 DR HSP; P04610; IJFW.  
 DR GO: GO:0042025; C:host cell nucleus; IEA.  
 DR GO: GO:0005634; C:nucleus; IEA.  
 DR GO: GO:0003723; F:RNA binding; IEA.  
 DR GO: GO:0003700; F:transcription factor activity; IEA.  
 DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro; IPR000345; CytC\_heme\_BS.  
 DR InterPro; IPR001831; IV\_Tat.  
 DR Pfam; PF00539; Tat; 1.  
 DR PROSITE; PS00190; CYTOCHROME C; UNKNOWN 1.  
 KW Activator; Nuclear protein; RNA-binding; Transcription;  
 KW Transcription regulation.  
 FT NON TER 71  
 SQ SEQUENCE 71 AA; 8226 MW; 324F908AF030E216 CRC64;  
 Query Match 100.0%; Score 58; DB 2; Length 71;  
 Best Local Similarity 100.0%; Pred. No. 0.018;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YGRKKRRQRRR 11  
 DB 47 YGRKKRRQRRR 57  
 RESULT 14  
 O40233 PRELIMINARY; PRT; 71 AA.  
 ID O40233  
 AC O40233  
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Tat protein (Fragment).  
 GN Name=tat;  
 OS Human immunodeficiency virus 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=HP93-Altat;  
 RX MEDLINE=97335179; PubMed=9191845; DOI=10.1006/viro.1997.8586;  
 RA Kirchhoff F., Greenough T.C., Hamacher M., Sullivan J.L.,  
 RA Desrosiers R.C.;  
 RT "Activity of human immunodeficiency virus type 1 promoter/TAR regions  
 RT and tat1 genes derived from individuals with different rates of  
 RT disease progression.";  
 RL Virology 232:319-331(1997).  
 CC -1- FUNCTION: Transcriptional regulator that acts by binding to the  
 CC trans-activating responsive sequence (TAR) RNA element and  
 CC activates transcription initiation and/or elongation from the LTR  
 CC promoter (By similarity).  
 DR EMEL; AF000529; AAB62528.1; -.  
 DR HSP; P04610; IJFW.  
 DR GO: GO:0042025; C:host cell nucleus; IEA.  
 DR GO: GO:0005634; C:nucleus; IEA.  
 DR GO: GO:0003723; F:RNA binding; IEA.  
 DR GO: GO:0003700; F:transcription factor activity; IEA.  
 DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro; IPR001831; IV\_Tat.  
 DR Pfam; PF00539; Tat; 1.  
 DR PRINTS; PR00055; HIVTATDOMAIN.  
 KW Activator; Nuclear protein; RNA-binding; Transcription;  
 KW Transcription regulation.  
 FT NON TER 71  
 SQ SEQUENCE 71 AA; 8162 MW; 5AFE3242E82321B3 CRC64;  
 Query Match 100.0%; Score 58; DB 2; Length 71;

Best Local Similarity 100.0%; Pred. No. 0.018;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YGRKKRRQRRR 11  
 DB 47 YGRKKRRQRRR 57  
 RESULT 13  
 O40232 PRELIMINARY; PRT; 71 AA.  
 ID O40232  
 AC O40232  
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Tat protein (Fragment).  
 GN Name=tat;  
 OS Human immunodeficiency virus 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=HP91-Altat;  
 RX MEDLINE=97335179; PubMed=9191845; DOI=10.1006/viro.1997.8586;  
 RA Kirchhoff F., Greenough T.C., Hamacher M., Sullivan J.L.,  
 RA Desrosiers R.C.;  
 RT "Activity of human immunodeficiency virus type 1 promoter/TAR regions  
 RT and tat1 genes derived from individuals with different rates of  
 RT disease progression.";  
 RL Virology 232:319-331(1997).  
 CC -1- FUNCTION: Transcriptional regulator that acts by binding to the  
 CC trans-activating responsive sequence (TAR) RNA element and  
 CC activates transcription initiation and/or elongation from the LTR  
 CC promoter (By similarity).  
 DR EMEL; AF000530; AAB62529.1; -.  
 DR HSP; P04610; IJFW.  
 DR GO: GO:0042025; C:host cell nucleus; IEA.  
 DR GO: GO:0005634; C:nucleus; IEA.  
 DR GO: GO:0003723; F:RNA binding; IEA.  
 DR GO: GO:0003700; F:transcription factor activity; IEA.  
 DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro; IPR000345; CytC\_heme\_BS.  
 DR InterPro; IPR001831; IV\_Tat.  
 DR Pfam; PF00539; Tat; 1.  
 DR PROSITE; PS00190; CYTOCHROME C; UNKNOWN 1.  
 KW Activator; Nuclear protein; RNA-binding; Transcription;  
 KW Transcription regulation.  
 FT NON TER 71  
 SQ SEQUENCE 71 AA; 8226 MW; 324F908AF030E216 CRC64;  
 Query Match 100.0%; Score 58; DB 2; Length 71;  
 Best Local Similarity 100.0%; Pred. No. 0.018;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YGRKKRRQRRR 11  
 DB 47 YGRKKRRQRRR 57  
 RESULT 14  
 O40233 PRELIMINARY; PRT; 71 AA.  
 ID O40233  
 AC O40233  
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Tat protein (Fragment).  
 GN Name=tat;  
 OS Human immunodeficiency virus 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.

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RC STRAIN=MR94-A3tat;
RX MEDLINE=97335179; PubMed=9191845; DOI=10.1006/viro.1997.8586;
RA Kirchhoff F., Greenough T.C., Hamacher M., Sullivan J.L.,
RA Desrosiers R.C.;
RT "Activity of human immunodeficiency virus type 1 promoter/TAR regions
RT and tat1 genes derived from individuals with different rates of
RT disease progression.";
RL Virology 232:319-331(1997).
CC -!- FUNCTION: Transcriptional regulator that acts by binding to the
CC trans-activating responsive sequence (TAR) RNA element and
CC activates transcription initiation and/or elongation from the LTR
CC promoter (By similarity).
CC EMBL; AF000531; AAB62530.1; -.
DR HSSP; P12506; 1TBC.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001831; IV_Tat.
DR Pfam; PF00539; Tat; 1.
KW Activator; Nuclear protein; RNA-binding; Transcription;
KW Transcription regulation.
FT NON_TER 71
SQ SEQUENCE 71 AA; 8034 MW; 5BBA79FB327EA3CD CRC64;

Query Match 100.0%; Score 58; DB 2; Length 71;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRKKRQRRR 11
DB 47 YGRKKRQRRR 57

RESULT 15
O40234
ID O40234 PRELIMINARY; PRT; 71 AA.
AC O40234;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Tat protein (Fragment).
GN Name=tat;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PC93-A2tat;
RX MEDLINE=97335179; PubMed=9191845; DOI=10.1006/viro.1997.8586;
RA Kirchhoff F., Greenough T.C., Hamacher M., Sullivan J.L.,
RA Desrosiers R.C.;
RT "Activity of human immunodeficiency virus type 1 promoter/TAR regions
RT and tat1 genes derived from individuals with different rates of
RT disease progression.";
RL Virology 232:319-331(1997).
CC -!- FUNCTION: Transcriptional regulator that acts by binding to the
CC trans-activating responsive sequence (TAR) RNA element and
CC activates transcription initiation and/or elongation from the LTR
CC promoter (By similarity).
CC EMBL; AF000532; AAB62531.1; -.
DR HSSP; P04610; 1JFW.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001831; IV_Tat.
DR Pfam; PF00539; Tat; 1.
KW Activator; Nuclear protein; RNA-binding; Transcription;
KW Transcription regulation.
FT NON_TER 71
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SQ SEQUENCE 71 AA; 8235 MW; A8030BF1E71A863D CRC64;

Query Match 100.0%; Score 58; DB 2; Length 71;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRKKRQRRR 11
DB 47 YGRKKRQRRR 57

Search completed: March 31, 2005, 00:30:52
Job time : 8.13461 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 31, 2005, 00:17:06 ; Search time 11.2 Seconds  
(without alignments)  
552.515 Million cell updates/sec

Title: US-10-049-822a-13  
Perfect score: 93  
Sequence: 1 RQIKWIFQNRMKWK 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*  
1: Geneseqp1980s:\*  
2: Geneseqp1990s:\*  
3: Geneseqp2000s:\*  
4: Geneseqp2001s:\*  
5: Geneseqp2002s:\*  
6: Geneseqp2003as:\*  
7: Geneseqp2003bs:\*  
8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	93	100.0	16	4	AAB73306 Drosophil
2	93	100.0	16	7	ADF56535 Homeobox
3	85	91.4	17	3	AY83570 Peptide f
4	84	90.3	16	2	AAW45974 Cysteine
5	84	90.3	16	2	AAW33407 Peptide 4
6	84	90.3	16	2	AAW33410 D-form pe
7	84	90.3	16	2	AAW82958 Oestrogen
8	84	90.3	16	2	AAW56397 Preferred
9	84	90.3	16	2	AAW71270 Antennape
10	84	90.3	16	2	AAW71316 Antennape
11	84	90.3	16	2	AAW30508 Drosophil
12	84	90.3	16	2	AAW91046 Internali
13	84	90.3	16	2	AY52102 Peptide f
14	84	90.3	16	2	AY00859 Peptide p
15	84	90.3	16	2	AY13509 Signal se
16	84	90.3	16	3	AY87920 Drosophil
17	84	90.3	16	3	AB27060 Beta-cate
18	84	90.3	16	3	AY93667 Peptide w
19	84	90.3	16	3	AY67966 Carboxyl
20	84	90.3	16	3	AY93551 Amino aci
21	84	90.3	16	3	AY55818 Signal se
22	84	90.3	16	3	AY71008 Drosophil
23	84	90.3	16	3	AY51212 Antennape
24	84	90.3	16	3	AY51167 Drosophil
25	84	90.3	16	3	AA10343 Peptide A

## ALIGNMENTS

RESULT.1  
AAB73306

ID AAB73306 standard; protein; 16 AA.

XX AC AAB73306;

DT 22-MAY-2001 (first entry)

DE Drosophila antennapedia protein transduction domain (PTD).

KW Antennapedia; protein transduction domain; PTD; fusion protein;

KW rat Bcl-xL mutant; Bcl-xFNK; apoptosis inhibitor; membrane permeable;

KW programmed cell death inhibitor; wild-type; antiapoptotic;

KW cell death-associated disease; tissue transplant preservative.

OS Drosophila sp.

XX WO200112807-AL.

XX 22-FEB-2001.

XX 17-AUG-2000; 2000WO-JP005502.

XX 17-AUG-1999; 99JP-00230842.

XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.

XX Ohta S, Asoh S;

XX WPI; 2001-211219/21.

Modified cDNA of rat bcl-x gene and encoded protein with membrane permeability to enhance uptake for effective inhibition of cell death e.g. apoptosis, useful in remedies for diseases associated with cell death.

Claim 3; Page 51; 56pp; Japanese.

The invention relates to a mutant rat Bcl-x protein and the cDNA encoding it. The mutant rat Bcl-x protein (Bcl-xFNK) has the substitutions Y22F, Q26N, and R165K relative to the wild-type Bcl-xL protein. The invention also encompasses recombinant vectors and host cells comprising the modified nucleic acid sequence. The mutant Bcl-x protein is able to permeate the cell membrane, thus enhancing its ability to be taken up into a cell and to act as an inhibitor of apoptosis (programmed cell death). Bcl-xFNK and nucleic acids encoding it are useful in remedies for diseases associated with cell death and in additives for maintaining the stability of transplanted cells and organs. The present sequence

26	84	90.3	16	3	AAB19251	Aab19251 Fragment
27	84	90.3	16	3	AA93178	Aay93178 Protegrin
28	84	90.3	16	3	AAB35694	Aab35694 Peptide a
29	84	90.3	16	3	AAB22025	Aab22025 Membrane
30	84	90.3	16	3	AAB29423	Aab29423 ANTP pept
31	84	90.3	16	3	AAB03927	Aab03927 Internali
32	84	90.3	16	3	AA93954	Aay93954 Peptide u
33	84	90.3	16	3	AAB29574	Aab29574 Antennape
34	84	90.3	16	3	ADE14785	Adel14785 Carrier m
35	84	90.3	16	3	ADE14761	Adel14761 Drosophil
36	84	90.3	16	4	AAB73091	Aab73091 Rheumatoi
37	84	90.3	16	4	AAB60004	Aab60004 Internali
38	84	90.3	16	4	AAB70753	Aab70753 Cell memb
39	84	90.3	16	4	AAE02974	Aae02974 Protein t
40	84	90.3	16	4	AAB60671	Aab60671 Antennape
41	84	90.3	16	4	AAU06064	Aau06064 Drosophil
42	84	90.3	16	4	AAB49914	Aab49914 HIF-1alph
43	84	90.3	16	4	AAB66996	Aab66996 Antennape
44	84	90.3	16	4	AAU00813	Aau00813 Fruit fly
45	84	90.3	16	4	AAE12205	Aae12205 Membrane

CC represents the Drosophila antennapedia protein transduction domain (PTD)  
 CC which is specifically claimed for use in generating Bcl-xFNK fusion  
 CC proteins  
 XX

SQ Sequence 16 AA;

Query Match 100.0%; Score 93; DB 4; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 6.7e-07;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RQIKWIFQNRMRKWKFK 16  
 |||||  
 Db 1 RQIKWIFQNRMRKWKFK 16

# RESULT 2

ID ADF56535 standard; peptide; 16 AA.

AC ADF56535;

XX 12-FEB-2004 (first entry)

DT Homeobox protein Antennapedia protein transduction domain, PTD, SEQ ID 4.

DE Human; synovial sarcoma; hBRM/hSNF2 alpha;  
 KW cytoplasmic membrane penetrating peptide; cytostatic;  
 KW protein transduction domain; PTD; homeobox; antennapedia.

XX Drosophila sp.

OS JP2003252802-A.

PN 10-SEP-2003.

XX 27-FEB-2002; 2002JP-00050894.

XX 27-FEB-2002; 2002JP-00050894.

XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.

XX WPI; 2003-857284/80.

XX Novel drug comprising hBRM/hSNF2 alpha polynucleotide, useful for  
 PT treating human synovial sarcoma.

XX Disclosure; SEQ ID NO 4; 21pp; Japanese.

CC The present invention relates to a drug (I) for treating human synovial  
 CC sarcoma by introducing into the cell the fusion protein hBRM/ hSNF2  
 CC (alpha) (II; ADF56533), or its coding sequence (ADF56532). (II) comprises  
 CC a cytoplasmic membrane penetrating peptide. (I) is useful for treating  
 CC human synovial sarcoma.

SQ Sequence 16 AA;

Query Match 100.0%; Score 93; DB 7; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 6.7e-07;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RQIKWIFQNRMRKWKFK 16  
 |||||  
 Db 1 RQIKWIFQNRMRKWKFK 16

# RESULT 3

ID AAY83570 standard; peptide; 17 AA.

XX AAY83570;

XX 29-AUG-2000 (first entry)

DT

XX

DE Peptide fragment of membrane transport vector penetratin.

XX Penetratin; translocation; membrane; drug delivery; therapy; treatment;  
 KW conjugate; vector.

XX Synthetic.

Key Location/Qualifiers  
 Modified-site 1  
 /label= Beta-alanine  
 /note= "Biotinylated"

XX WO200029427-A2.

XX 25-MAY-2000.

XX 11-NOV-1999; 99WO-GB003750.

XX 13-NOV-1998; 98GB-00025000.

XX 13-NOV-1998; 98GB-00025001.

XX 04-FEB-1999; 99GB-00002522.

XX 04-FEB-1999; 99GB-00002525.

XX 22-JUN-1999; 99GB-00014578.

XX (CYCL-) CYCLACEL LTD.

XX Fischer MP, Zhelev N;

XX WPI; 2000-387734/33.

XX New membrane translocation peptide carrier group for delivering

XX therapeutic agents into target cells comprises specified sequence of

XX amino acids.

XX Claim 9; Page 27; 59pp; English.

XX Penetratin is a membrane translocation polypeptide and as such, active  
 CC peptide fragments of penetratin can be used to translocate conjugated  
 CC molecules across the cell membrane e.g. drugs. 13 chemical entities are  
 CC described for use in the method such as pacifitaxel-  
 CC 2'succinimidopropionyl CbetAA-RRMKWK-NH 2, and podophyllotoxin-4-  
 CC succinimidopropionyl CbetAA-RRMKWK-NH 2. The method has applications as  
 CC a drug delivery system for treatment and therapy. The resulting  
 CC conjugated molecules exhibit high immunogenicity, solubility and  
 CC clearance. The penetratin peptide fragment may be truncated and or have  
 CC amino acid substitutions. See GENESEQ records AAY83520-Y83581

XX Sequence 17 AA;

Query Match 91.4%; Score 85; DB 3; Length 17;

Best Local Similarity 93.8%; Pred. No. 1.1e-05;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RQIKWIFQNRMRKWKFK 16  
 |||||  
 Db 2 RQIKWIFQNRMRKWKAK 17

# RESULT 4

AAY45974

ID AAY45974 standard; peptide; 16 AA.

XX AAY45974;

XX 01-JUL-1998 (first entry)

XX Cysteine protease inhibiting peptide for preventing cell death.

XX Neuronal cell death; neurodegenerative disorder; inhibition;

XX cysteine protease; cardiovascular; liver disease.

XX Synthetic.



```

FH Key                               Location/Qualifiers
FT Modified-site 1
FT                                     /note= "N-3-nitro-2-pyridyl-sulphenyl-Arg"
XX
XX
XX WO9735876-A1.
XX
XX 02-OCT-1997.
XX
XX 04-MAR-1997; 97WO-US004158.
XX
XX 04-MAR-1996; 96US-00610220.
XX
XX (UYCO ) UNIV COLUMBIA NEW YORK.
XX
XX Troy CM;
XX
XX WPT; 1997-489561/45.
XX
XX New cysteine protease inhibiting peptide(s) for preventing cell death -
XX in cases of neurodegenerative, cardiovascular and liver diseases, and
XX their peptido-mimetics, and general method for identifying enzyme
XX inhibiting peptides.
XX
XX Claim 8; Page 68; 112pp; English.
XX
XX This sequence represents a specifically claimed peptide of the formula: V
XX -(AA1)n-Cys(V')-(AA2)m-V' (I), in which n and m = 0-5, totalling 2-5; if
XX n = 1, AA1 = Ala; if n = 2, (AA1)n = Gln-Ala; and if n = 3 or more, (AA1)n
XX = (X)p-Gln-Ala; X = any amino acid; p = 1-3, depending on value of n; if
XX m = 1, AA2 = Arg; if m = 2, (AA2)n = Arg-Gly; if m = 3 or more, (AA2)n =
XX Arg-Gly-(X)q; q = 1-3, depending on value of m; V, V' and V'', any or all
XX of which may be absent, = agent able to direct the compound to a specific
XX cell. The peptides are inhibitors of cysteine proteases, specifically
XX interleukin-1 beta converting enzyme (ICE). They inhibit death of cells,
XX particularly in humans, and can be used to treat neurodegenerative
XX diseases (e.g. ageing, Alzheimer's, Machado-Joseph, Parkinson's or
XX Huntington's diseases, multiple sclerosis, muscular dystrophy, stroke),
XX cardiovascular disease and liver disorders. The peptides should be more
XX specific than pseudosubstrate inhibitors
XX
XX Sequence 16 AA;
XX
XX Query Match 90.3%; Score 84; DB 2; Length 16;
XX Best Local Similarity 93.8%; Pred. No. 1.4e-05;
XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX Qy 1 RQIKWQNRRMKWFK 16
XX |||||
XX Db 1 RQIKWQNRRMKWKK 16
XX
XX RESULT 5
XX AAW33407
XX ID AAW33407 standard; peptide; 16 AA.
XX
XX AC AAW33407;
XX
XX DT 27-AUG-2003 (revised)
XX DT 17-MAR-1998 (first entry)
XX
XX DE Peptide 43-58 of homeodomain Antp.
XX
XX KW homeodomain; transcription factor; Antennapedia; Antp; vector;
XX transfection; hydrophobic.
XX
XX OS Unidentified.
XX
XX FN WO9712912-A1.
XX
XX PD 10-APR-1997.
XX
XX PF 04-OCT-1996; 96WO-FR001553.
XX
XX PR 05-OCT-1995; 95FR-00011714.
XX
XX PA (CNRS ) CNRS CENT NAT RECH SCI.
XX
XX
XX PR 05-OCT-1995; 95FR-00011714.
XX
XX PA (CNRS ) CNRS CENT NAT RECH SCI.
XX
XX Chassaing G, Prochiantz A;
XX
XX WPT; 1997-226166/20.
XX
XX New peptide(s) of high hydrophobic amino acid content - useful as vectors
XX for delivering peptides and nucleic acids to cells.
XX
XX Claim 1; Page 7; 35pp; French.
XX
XX New peptides are provided which are 16 amino acids long and which are
XX analogues of the peptide corresponding to residues 43-58 of the
XX Antennapedia transcription factor homeodomain (AntpHD). The peptides
XX contain 6-10 hydrophobic amino acids. They have the general formula: X1-
XX X2-X3-X4-X5-Trp-X7-X8-X9-X10-X11-X12-X13-X14-X15-X16 or X16-X15-X14-X13-
XX X12-X11-X10-X9-X8-X7-Trp-X5-X4-X3-X2-X1 in which X1-X5 and X7-X16 are any
XX alpha-amino acids, provided that: (1) the peptide contains 6-10
XX hydrophobic amino acids; (2) X3 and X5 are not both Val; and (3) the
XX natural Antp 43-58 sequence RQIKWQNRRMKWKK (i.e. the present sequence)
XX is excluded. Specific examples of these peptides are given in AAW3408 -
XX AAW3416. The peptides are used as vectors for introducing into live
XX cells compounds which affect cell function, esp. peptides and nucleic
XX acids. They can cross cellular membranes and reach various cell
XX compartments. They are as effective as helix 3 of a homeodomain peptide.
XX (Updated on 27-AUG-2003 to correct OS field.)
XX
XX Sequence 16 AA;
XX
XX Query Match 90.3%; Score 84; DB 2; Length 16;
XX Best Local Similarity 93.8%; Pred. No. 1.4e-05;
XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX Qy 1 RQIKWQNRRMKWFK 16
XX |||||
XX Db 1 RQIKWQNRRMKWKK 16
XX
XX RESULT 6
XX AAW33410
XX ID AAW33410 standard; peptide; 16 AA.
XX
XX AC AAW33410;
XX
XX DT 17-MAR-1998 (first entry)
XX
XX DE D-form peptide 43-58 of homeodomain Antp.
XX
XX KW homeodomain; transcription factor; Antennapedia; Antp; vector;
XX transfection; hydrophobic.
XX
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers
XX FT Misc-difference 1..16
XX FT Modified-site 1 /note= "all residues are D-form"
XX
XX FT /note= "in determining the ability of this sequence to be
XX internalised in cells, a biotin-aminopentanoyl group was
XX attached to the N-terminal"
XX
XX FN WO9712912-A1.
XX
XX PD 10-APR-1997.
XX
XX PF 04-OCT-1996; 96WO-FR001553.
XX
XX PR 05-OCT-1995; 95FR-00011714.
XX
XX PA (CNRS ) CNRS CENT NAT RECH SCI.
XX
XX

```

PI Chassaing G, Prochiantz A;  
 DR WPI; 1997-226166/20.  
 XX  
 XX New peptide(s) of high hydrophobic amino acid content - useful as vectors  
 PT for delivering peptides and nucleic acids to cells.  
 XX  
 XX Disclosure; Page 7; 35pp; French.  
 XX  
 XX New peptides are provided which are 16 amino acids long and which are  
 CC analogues of the peptide corresponding to residues 43-58 of the  
 CC Antennapedia transcription factor homeodomain (AntpHD). The peptides  
 CC contain 6-10 hydrophobic amino acids. They have the general formula: X1-  
 CC X2-X3-X4-X5-Trp-X7-X8-X9-X10-X11-X12-X13-X14-X15-X16 or X16-X15-X14-X13-  
 CC X12-X11-X10-X9-X8-X7-Trp-X5-X4-X3-X2-X1 in which X1-X5 and X7-X16 are any  
 CC alpha-amino acids, provided that: (1) the peptide contains 6-10  
 CC hydrophobic amino acids; (2) X3 and X5 are not both Val; and (3) the  
 CC natural Antp 43-58 sequence RQIKWFWQRMRMKWK (see AAW33407) is excluded.  
 CC The present sequence (the D-form of the 43-58 peptide) is a specific  
 CC example of the new peptides. The peptides are used as vectors for  
 CC introducing into live cells compounds which affect cell function,  
 CC especially peptides and nucleic acids. They can cross cellular membranes  
 CC and reach various cell compartments. They are as effective as helix 3 of  
 CC a homeodomain peptide  
 XX  
 XX Sequence 16 AA;  
 SQ  
 Query Match 90.3%; Score 84; DB 2; Length 16;  
 Best Local Similarity 93.8%; Pred. No. 1.4e-05;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 RQIKWFWQRMRMKWK 16  
 DB 1 RQIKWFWQRMRMKWK 16  
 RESULT 7  
 AAW82958  
 ID AAW82958 standard; peptide; 16 AA.  
 XX  
 XX AAW82958;  
 AC  
 XX 04-FEB-1999 (first entry)  
 DT  
 XX  
 DE Oestrogen receptor activity inhibiting peptide #14.  
 XX  
 XX Human; oestrogen receptor activity inhibitor; anti-oestrogen; diagnosis;  
 KW breast cancer; estrogen; tumour; phosphotyrosyl peptide;  
 KW malonyltyrosyl peptide; steroid receptor co-activator-1.  
 XX  
 XX Synthetic.  
 OS Homo sapiens.  
 XX  
 XX WO9846250-A1.  
 PN  
 XX 22-OCT-1998.  
 PD  
 XX 14-APR-1998; 98WO-US007711.  
 PP  
 XX 14-APR-1997; 97US-0043545P.  
 PR  
 XX (REGC ) UNIV CALIFORNIA.  
 PA  
 XX Pietras RJ;  
 PI  
 XX WPI; 1998-594522/50.  
 DR  
 XX New anti-oestrogen peptide compositions - comprise sequences based on  
 PT oestrogen receptor and steroid receptor co-activator-1 sequences, used  
 PT for treating cancers.  
 XX  
 XX Claim 59; Page 156; 182pp; English.  
 PS  
 XX  
 CC The present invention describes a composition comprising an isolated  
 CC oestrogen receptor activity inhibiting (anti-oestrogen) peptide. The  
 CC peptides used in the composition comprise sequences of human oestrogen  
 CC receptor (OR) surrounding Tyr537 and steroid receptor co-activator-1 (SRC  
 CC -1). The peptide compositions, nucleic acids and vectors of the present  
 CC invention can reduce OR activity in a cell, reduced OR polypeptide  
 CC dimerisation in a cell and reduce the binding of SRC-1 polypeptide to an  
 CC OR polypeptide dimer in a cell. They can be used for killing cancer cells  
 CC and treating cancers, particularly breast cancer. The present sequence  
 CC represents a specifically claimed anti-oestrogen peptide  
 XX  
 XX Sequence 16 AA;  
 SQ  
 Query Match 90.3%; Score 84; DB 2; Length 16;  
 Best Local Similarity 93.8%; Pred. No. 1.4e-05;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 RQIKWFWQRMRMKWK 16  
 DB 1 RQIKWFWQRMRMKWK 16  
 RESULT 8  
 AAW56397  
 ID AAW56397 standard; peptide; 16 AA.  
 XX  
 XX AAW56397;  
 AC  
 XX 05-AUG-1998 (first entry)  
 DT  
 XX  
 DE Preferred signal sequence of the invention.  
 XX  
 XX Signal peptide; nuclear localisation signal; NLS;  
 KW immunosuppressive activity; inhibition; nuclear translocation inhibitor;  
 KW nuclear translocation; treatment; immune disorder; autoimmune disease;  
 KW hypersensitivity; sepsis; prevention; septic shock; antiviral agent;  
 KW tumour growth suppressor.  
 XX  
 XX Unidentified.  
 OS  
 XX WO9811907-A1.  
 PN  
 XX 26-MAR-1998.  
 PD  
 XX 15-SEP-1997; 97WO-US016217.  
 PF  
 XX 20-SEP-1996; 96US-0026978P.  
 PR  
 XX 12-SEP-1997; 97US-00928958.  
 PP  
 XX (BRIM ) BRISTOL-MYERS SQUIBB CO.  
 PA  
 XX Nadler SG, Cleaveland JS, Blake J, Haffar OK;  
 PI WPI; 1998-217028/19.  
 DR  
 XX Nuclear translocation inhibitor polypeptides - comprising signal sequence  
 PT for delivery through the cytoplasmic membrane and at least 2 nuclear  
 PT localisation sequences.  
 XX  
 XX Claim 5; Page 43; 69pp; English.  
 PS  
 XX Peptides AAW56397-99 represent preferred signal sequences of the  
 CC invention. They are used to construct the nuclear translocation inhibitor  
 CC polypeptides of the invention. Nuclear translocation inhibitor  
 CC polypeptides comprise a signal sequence peptide capable of delivering the  
 CC polypeptide through the cytoplasmic membrane into a cell, and at least 2  
 CC nuclear localisation signals (NLSs). The polypeptides can be used to  
 CC inhibit nuclear translocation of a cellular protein. In addition, since  
 CC the nuclear translocation of certain cellular peptides is required for  
 CC the host organism to mount an immune response, the polypeptide inhibitors  
 CC are useful as immunosuppression agents. The polypeptides can therefore be  
 CC used for the treatment of immune disorders including autoimmune diseases.  
 CC The polypeptides can also be used for treating physical symptoms

CC manifested by responses to allergens which can initiate a state of  
 CC hypersensitivity, for the treatment of sepsis and in the prevention of  
 CC septic shock, antiviral agents, tumour growth suppressors, and for  
 CC transcriptionally modulating the expression of cellular genes  
 XX SQ Sequence 16 AA;

Query Match 90.3%; Score 84; DB 2; Length 16;  
 Best Local Similarity 93.8%; Pred. NO. 1.4e-05;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ROIKIWFQNRMRKWKPK 16  
 DB 1 ROIKIWFQNRMRKWKPK 16

RESULT 9  
 AAW71270  
 ID AAW71270 standard; protein; 16 AA.  
 XX AC AAW71270;  
 XX DT 23-NOV-1998 (first entry)  
 XX DE Antennapedia peptide for directing antisense oligonucleotides to a cell.  
 XX KW Antisense oligonucleotide; inhibit; cell death; Nedd2; human Ich-1L gene;  
 KW neuronal cell death; treatment; aging; amyotrophic lateral sclerosis;  
 KW Alzheimer's disease; dentatorubral; pallidolysial atrophy;  
 KW Huntington's disease; Machado-Joseph disease; multiple sclerosis;  
 KW muscular dystrophy; Parkinson's disease; senility;  
 KW spinocerebellar ataxia type I; spinobulbar muscular atrophy; stroke;  
 KW trauma; antennapedia.  
 XX OS Synthetic.  
 XX FH Key Location/Qualifiers  
 XX FT Modified-site 1  
 XX FT /note= "N-terminal protected with 3-nitro-2-pyridyl  
 XX FT sulphenyl group (Npys)"  
 XX PN WO9838861-A1.  
 XX PD 11-SEP-1998.  
 XX PF 03-MAR-1998; 98WO-US004128.  
 XX PR 03-MAR-1997; 97US-00810540.  
 XX PA (UYCO ) UNIV COLUMBIA NEW YORK.  
 XX PI Troy CM, Shelanski ML;  
 XX DR WPI; 1998-506333/43.  
 XX PT Anti-sense oligonucleotide(s) to cysteine aspartase genes - used to  
 PT inhibit neurodegenerative disorder associated with e.g. ageing,  
 PT Alzheimer's, Huntington's or Parkinson's disease.  
 XX PS Claim 5; Page 39; 60pp; English.  
 XX CC AAW71270 and AAW71315-16 represent antennapedia peptides which are used  
 CC to, direct the antisense oligonucleotides (AAV54973-74) of the invention  
 CC to a cell. The antisense oligonucleotides are used to inhibit cell death  
 CC mediated by withdrawal of a trophic factor. AAV54973 inhibits the  
 CC expression of a Nedd2 rodent gene, while AAV54974 inhibits expression of  
 CC a human Ich-1L gene. The oligonucleotides are used to inhibit neuronal  
 CC cell death, especially for treatment of neuronal cell death caused by  
 CC e.g. aging, amyotrophic lateral sclerosis, Alzheimer's disease,  
 CC dentatorubral and pallidolysial atrophy, Huntington's disease, Machado-  
 CC Joseph disease, multiple sclerosis, muscular dystrophy, Parkinson's  
 CC disease, senility, spinocerebellar ataxia type I, spinobulbar muscular  
 CC atrophy, stroke or trauma

XX SQ Sequence 16 AA;  
 Query Match 90.3%; Score 84; DB 2; Length 16;  
 Best Local Similarity 93.8%; Pred. NO. 1.4e-05;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ROIKIWFQNRMRKWKPK 16  
 DB 1 ROIKIWFQNRMRKWKPK 16

RESULT 10  
 AAW71316  
 ID AAW71316 standard; protein; 16 AA.  
 XX AC AAW71316;  
 XX DT 23-NOV-1998 (first entry)  
 XX DE Antennapedia peptide for directing antisense oligonucleotides to a cell.  
 XX KW Antisense oligonucleotide; inhibit; cell death; Nedd2; human Ich-1L gene;  
 KW neuronal cell death; treatment; aging; amyotrophic lateral sclerosis;  
 KW Alzheimer's disease; dentatorubral; pallidolysial atrophy;  
 KW Huntington's disease; Machado-Joseph disease; multiple sclerosis;  
 KW muscular dystrophy; Parkinson's disease; senility;  
 KW spinocerebellar ataxia type I; spinobulbar muscular atrophy; stroke;  
 KW trauma; antennapedia.  
 XX OS Synthetic.  
 XX FH Key Location/Qualifiers  
 XX FT Modified-site 1  
 XX FT /note= "N-terminal protected with 3-nitro-2-pyridyl  
 XX FT sulphenyl group (Npys)"  
 XX PN WO9838861-A1.  
 XX PD 11-SEP-1998.  
 XX PF 03-MAR-1998; 98WO-US004128.  
 XX PR 03-MAR-1997; 97US-00810540.  
 XX PA (UYCO ) UNIV COLUMBIA NEW YORK.  
 XX PI Troy CM, Shelanski ML;  
 XX DR WPI; 1998-506333/43.  
 XX PT Anti-sense oligonucleotide(s) to cysteine aspartase genes - used to  
 PT inhibit neurodegenerative disorder associated with e.g. ageing,  
 PT Alzheimer's, Huntington's or Parkinson's disease.  
 XX PS Disclosure; Page 14; 60pp; English.  
 XX CC AAW71270 and AAW71315-16 represent antennapedia peptides which are used  
 CC to, direct the antisense oligonucleotides (AAV54973-74) of the invention  
 CC to a cell. The antisense oligonucleotides are used to inhibit cell death  
 CC mediated by withdrawal of a trophic factor. AAV54973 inhibits the  
 CC expression of a Nedd2 rodent gene, while AAV54974 inhibits expression of  
 CC a human Ich-1L gene. The oligonucleotides are used to inhibit neuronal  
 CC cell death, especially for treatment of neuronal cell death caused by  
 CC e.g. aging, amyotrophic lateral sclerosis, Alzheimer's disease,  
 CC dentatorubral and pallidolysial atrophy, Huntington's disease, Machado-  
 CC Joseph disease, multiple sclerosis, muscular dystrophy, Parkinson's  
 CC disease, senility, spinocerebellar ataxia type I, spinobulbar muscular  
 CC atrophy, stroke or trauma  
 XX SQ Sequence 16 AA;

Query Match 90.3%; Score 84; DB 2; Length 16;

```

Best Local Similarity 93.8%; Pred. NO. 1.4e-05;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RQIKIWQNRRMKWFK 16
Db 1 RQIKIWQNRRMKWKK 16

RESULT 11
AAW30508
ID AAW30508 standard; peptide; 16 AA.
XX
AC AAW30508;
XX
DT 26-OCT-1998 (first entry)
XX
DE Drosophila membrane translocation sequence.
XX
KW DP-1; transcription factor; antagonist; E2F protein; apoptosis;
KW cell proliferation; cardiovascular cell; restenosis; tumour;
KW surgical stent; therapy; membrane translocation; antennapedia protein.
XX
KW Drosophila melanogaster.
OS
XX
FN WO9828334-A1.
XX
PD 02-JUL-1998.
XX
PF 22-DEC-1997; 97WO-GB003506.
XX
PR 20-DEC-1996; 96GB-00026589.
XX
PA (PROL-) PROLIFIX LTD.
XX
PI La Thangue NB, Bandara LR;
XX
DR WPI; 1998-377596/32.
XX
PT Polypeptide fragments of the DP-1 transcription factor - used for
PT inducing apoptosis, specifically in tumour and cardiovascular cells, e.g.
PT for preventing re-stenosis.
XX
PS Disclosure; Page 5; 55pp; English.
XX
CC This polypeptide comprises a membrane translocation sequence derived from
CC the Drosophila melanogaster antennapedia protein. Such membrane
CC translocation sequences are useful in directing entry of a polypeptide
CC into a cell. Polypeptides of the invention (see AAW30504-07) are derived
CC from the DEF box region (see AAW30501) of transcription factor DP1. They
CC act as antagonists of the heterodimerisation of a DP protein with an E2F
CC protein, and can be used to induce apoptosis, specifically in tumour and
CC cardiovascular cells, e.g. for preventing restenosis. A claimed fusion
CC protein comprises a DEF box peptide and the Drosophila antennapedia
CC protein membrane translocation sequence
SQ
Sequence 16 AA;

Query Match 90.3%; Score 84; DB 2; Length 16;
Best Local Similarity 93.8%; Pred. NO. 1.4e-05;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RQIKIWQNRRMKWFK 16
Db 1 RQIKIWQNRRMKWKK 16

RESULT 12
AAW91046
ID AAW91046 standard; peptide; 16 AA.
XX
AC AAW91046;
XX
DT 24-MAR-1999 (first entry)
XX

Internalization sequence associated with cadherin modulating agents.

Alpha-catenin; beta-catenin; interaction; modulation; cell adhesion;
cadherin-mediated function; demyelinating neurological disease;
multiple sclerosis; drug delivery; cancer; angiogenesis; immune system;
central nervous system; apoptosis induction; cadherin-expression cell;
pregnancy prevention; vasopermeability; synaptic stability; diabetes;
rheumatoid arthritis; allergic response; learning; antennapedia protein;
antibody-mediated graft rejection; internalization sequence; memory.

Synthetic.
WO9845319-A2.
15-OCT-1998.
14-APR-1998; 98WO-CA000322.
10-APR-1997; 97US-0043361P.
(UTMC-) UNIV MCGILL.
Blaschuk OW, Gour BJ;
WPI; 1999-024009/02.
New catenin modulating agents - comprising peptides having a sequence HAV
or analogues or antibodies, used for modulating cadherin-mediated
functions.
Claim 16; Page 78; 106pp; English.

The present sequence represents antennapedia protein derived
internalization sequence associated with cadherin modulating agents.
These agents are used for modulating cadherin-mediated functions. They
can be used for disrupting interaction between alpha-catenin and beta-
catenin in a cell, inhibiting cell adhesion, e.g. between epithelial
cells, endothelial cells, neural cells, tumour cells and lymphocytes, for
treating a demyelinating neurological disease, e.g. multiple sclerosis,
for reducing unwanted cellular adhesion in a mammal, for enhancing the
delivery of a drug through the skin of a mammal, for enhancing the
delivery of a drug to a tumour in a mammal, for treating cancer in a
mammal, for inhibiting angiogenesis in a mammal, for enhancing drug
delivery to the central nervous system of a mammal, for inducing
apoptosis in a cadherin-expression cell, for modulating the immune system
of a mammal, for preventing pregnancy in a mammal, for increasing
vasopermeability in a mammal, or for inhibiting synaptic stability in a
mammal. In particular they can be used for treating diabetes, rheumatoid
arthritis, allergic responses, antibody-mediated graft rejection or for
stimulating learning and memory
SQ
Sequence 16 AA;

Query Match 90.3%; Score 84; DB 2; Length 16;
Best Local Similarity 93.8%; Pred. NO. 1.4e-05;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RQIKIWQNRRMKWFK 16
Db 1 RQIKIWQNRRMKWKK 16

RESULT 13
AAW52102
ID AAW52102 standard; peptide; 16 AA.
XX
AC AAW52102;
XX
DT 28-JAN-2000 (first entry)
XX
DE Peptide from the third helix of antennapedia homeodomain protein.
XX

```

KW Rho binding region; Rho binding protein; ROCK II; ROCK I; Kinection;  
 KW ROCK/Kinection homology domain; cell growth; assay; Skn 7; modulator;  
 KW antifungal agent; antennapedia homeodomain protein; translocate.  
 XX  
 OS Drosophila melanogaster.  
 XX  
 PN WO9952941-A2.  
 XX  
 XX 21-OCT-1999.  
 PD  
 XX  
 XX 09-APR-1999; 99WO-GB001096.  
 PF  
 XX  
 XX 09-APR-1998; 98GB-00007848.  
 PR  
 XX  
 XX (MEDI-) MEDICAL RES COUNCIL.  
 PA (IMCR ) IMPERIAL CANCER RES TECHNOLOGY.  
 XX  
 XX Johnston LH, Treisman RH;  
 PI  
 XX WPI; 1999-620374/53.  
 DR  
 XX  
 XX Assay for modulators of binding of Rho protein with its binding partners,  
 PT potentially useful as antifungal agents.  
 XX  
 XX Disclosure; Page 16; 69pp; English.  
 PS  
 XX This sequence is a peptide from the third helix of the Drosophila  
 CC antennapedia protein that translocates across biological membranes. This  
 CC sequence can be linked to the Rho binding region of the invention  
 CC (AAY52100) to cause translocation across eukaryotic cell membranes. The  
 CC Rho binding region is present in many Rho binding proteins, such as ROCK-  
 CC I, ROCK-II and Kinection and is also referred to as the ROCK/Kinection  
 CC homology domain. Rho-A is involved in many cellular processes including  
 CC stress fibre formation, cell motility, cytokinesis and apoptosis. The Rho  
 CC binding domain is used in the invention which relates to an assay for  
 CC potential modulators of cell growth. The assay consists of a Skn7  
 CC polypeptide, a beta2 polypeptide or a polypeptide consisting of a  
 CC ROCK/Kinection homology domain, a Rho polypeptide which binds to the  
 CC previous peptide and a test compound. The modulation of the binding of  
 CC the two peptides caused by the test compound is measured. The method is  
 CC used to identify modulators, particularly antagonists, of the interaction  
 CC of Rho with its binding partners, e.g. to render pathogens sensitive to  
 CC the host's defence system, particularly as antifungal agents. The  
 CC ROCK/Kinection homology domain can be used to screen databases for other  
 CC Rho-binding proteins  
 XX  
 XX Sequence 16 AA;  
 SQ

Query Match 90.3%; Score 84; DB 2; Length 16;  
 Best Local Similarity 93.8%; Pred. NO. 1.4e-05;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RQIKIWFQNRRMKWFK 16  
 |||||  
 DB 1 RQIKIWFQNRRMKWKK 16  
 |||||

RESULT 14  
 AAY00859  
 ID AAY00859 standard; peptide; 16 AA.  
 XX  
 AC AAY00859;  
 XX  
 XX 20-MAY-1999 (first entry)  
 DT  
 XX  
 XX Peptide pAntp(43-58) used in membrane-permeable construct.  
 DE  
 XX  
 XX Membrane-permeable construct; lipid membrane; membrane transport;  
 KW oligonucleotide delivery; cancer therapy; signal transduction; inhibitor;  
 KW gene therapy; transcription; translation; expression; replication.  
 XX  
 XX Synthetic.  
 OS  
 XX

FH Key Location/Qualifiers  
 FT Modified-site 16  
 FT /note= "amidated"  
 XX  
 XX WO9905302-A1.  
 XX  
 XX 04-FEB-1999.  
 XX  
 XX 16-JUL-1998; 98WO-US014761.  
 XX  
 XX 24-JUL-1997; 97US-0053678P.  
 XX  
 XX (PEKE ) PERKIN-ELMER CORP.  
 XX  
 XX Langel U, Bartfai T, Pooga M, Valkna A, Saar X, Hallbrink M;  
 PI  
 XX WPI; 1999-142952/12.  
 DR  
 XX  
 XX New membrane-permeable constructs - comprise a peptide linked by a labile  
 PT bond to a nucleic acid analogue capable of hybridising with an  
 FT intracellular polynucleotide.  
 XX  
 XX Disclosure; Page 26; 60pp; English.  
 PS  
 XX This sequence represents a peptide used in the construct of the  
 CC invention. The construct is a membrane-permeable construct for transport  
 CC across a lipid membrane, which comprises: (a) a nucleic acid analogue  
 CC capable of hybridising with an intracellular polynucleotide (PN); (b) a  
 CC peptide; and (c) a labile bond linking the nucleic acid analogue and the  
 CC peptide. The membrane-permeable constructs can be used for delivery of  
 CC oligonucleotides, nucleic acids and nucleic acid analogues into cells.  
 CC They can be used for e.g. cancer therapy, signal transduction studies,  
 CC identifying new intracellular drug targets or gene therapy. They can also  
 CC be used for selectively inhibiting DNA transcription, RNA translation,  
 CC RNA or DNA expression, DNA replication, or an DNA or RNA regulatory  
 CC function of preselected DNA or RNA sequences in a living cell  
 XX  
 XX Sequence 16 AA;  
 SQ

Query Match 90.3%; Score 84; DB 2; Length 16;  
 Best Local Similarity 93.8%; Pred. NO. 1.4e-05;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RQIKIWFQNRRMKWFK 16  
 |||||  
 DB 1 RQIKIWFQNRRMKWKK 16  
 |||||

RESULT 15  
 AAY13509  
 ID AAY13509 standard; peptide; 16 AA.  
 XX  
 XX AAY13509;  
 AC  
 XX 30-JUL-1999 (first entry)  
 DT  
 XX  
 XX Signal sequence of antennapedia.  
 DE  
 XX  
 XX Fusion protein; calpastatin; calpain; platelet aggregation; arthritis;  
 KW hypoxia; erythrocyte sickling; sickle cell; HIV provirus; NF-kappaB;  
 KW inflammation; asthma; immune response; restenosis; myocardial infarction;  
 KW cancer; calpastat; antennapedia.  
 XX  
 XX Mammalia.  
 OS  
 XX WO9922756-A1.  
 PN  
 XX  
 XX 14-MAY-1999.  
 PD  
 XX 04-NOV-1998; 98WO-US023526.  
 PF  
 XX  
 XX 04-NOV-1997; 97US-00964302.  
 PR  
 XX

PA (NEW-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.

PI Potter DA, Skolnik PR;

DR WPI; 1999-326923/27.

PT Fusion protein of signal sequence and calpastatin.

PS Disclosure; Page 5; 46pp; English.

XX The invention features fusion proteins that contain a calpastatin peptide  
 CC and a signal sequence capable of delivering the fusion protein into a  
 CC eukaryotic cell. The fusion protein is used for the inhibition of calpain  
 CC in a cell. The fusion proteins are specifically used: (a) to prevent  
 CC aggregation and degranulation of platelets (e.g. during storage); (b) to  
 CC inhibit hypoxia-induced sickling of erythrocytes (during storage,  
 CC facilitating subsequent transfusion of autologous cells for treatment of  
 CC sickle cell crises); and (c) to inhibit activation of human immune  
 CC deficiency virus provirus in infected cells (or similarly for other  
 CC viruses regulated by NP-kappaB). Other disclosed uses are: to treat or  
 CC prevent inflammation (e.g. arthritis or asthma), unwanted immune  
 CC responses (e.g. transplant rejection), restenosis (associated with  
 CC angioplasty), cancer, subarachnoid hemorrhage, vasospasm, muscular  
 CC dystrophy, cataracts and traumatic birth injury; to prevent spread of  
 CC platelets on surfaces (e.g. when applied to the surface of stents,  
 CC catheters etc.); to reduce coronary thrombosis in by-pass surgery and  
 CC angioplasty; to treat myocardial infarction, or to prevent progression of  
 CC infarction (myocardial or cerebral). The fusion protein has a reversible  
 CC inhibitory effect and enters cells easily. It allows platelets to be  
 CC stored cold with reduced change in shape

SQ Sequence 16 AA;

Query Match 90.3%; Score 84; DB 2; Length 16;  
 Best Local Similarity 93.8%; Pred. NO. 1.4e-05;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RQIKIWQNRMRKWK 16  
 |||||  
 Db 1 RQIKIWQNRMRKWK 16

Search completed: March 31, 2005, 00:28:25  
 Job time : 15.2 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 31, 2005, 00:23:16 ; Search time 3.2 Seconds  
(without alignments)  
373.245 Million cell updates/sec

Title: US-10-049-822a-13

Perfect score: 93

Sequence: 1 RQKIWFQNRKMKFK 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.\*

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6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	84	90.3	16	2	US-08-928-958-7
2	84	90.3	16	2	US-08-810-540-3
3	84	90.3	16	2	US-08-810-540-6
4	84	90.3	16	2	US-09-072-429-7
5	84	90.3	16	3	US-08-964-302A-6
6	84	90.3	16	3	US-09-116-294-4
7	84	90.3	16	3	US-08-964-614A-4
8	84	90.3	16	3	US-08-849-486-1
9	84	90.3	16	3	US-08-849-486-4
10	84	90.3	16	3	US-09-208-966-54
11	84	90.3	16	3	US-09-308-935-8
12	84	90.3	16	3	US-09-441-416A-6
13	84	90.3	16	3	US-09-296-089-33
14	84	90.3	16	3	US-09-419-826-35
15	84	90.3	16	3	US-09-302-305C-10
16	84	90.3	16	4	US-09-346-847-1
17	84	90.3	16	4	US-09-346-847-25
18	84	90.3	16	4	US-09-057-363C-47
19	84	90.3	16	4	US-09-043-560B-3
20	84	90.3	16	4	US-09-648-400A-29
21	84	90.3	16	4	US-09-227-652B-4
22	84	90.3	16	4	US-09-780-070-38
23	84	90.3	16	4	US-08-610-220B-9
24	84	90.3	16	4	US-09-775-052A-54
25	84	90.3	16	4	US-09-155-165-22
26	84	90.3	16	4	US-09-792-480-29
27	84	90.3	16	4	US-09-551-976-33

28	84	90.3	16	4	US-09-265-107-47	Sequence 47, Appl
29	84	90.3	16	4	US-09-707-263A-2	Sequence 2, Appl
30	84	90.3	16	4	US-09-545-433-9	Sequence 9, Appl
31	84	90.3	16	4	US-09-720-003C-4	Sequence 4, Appl
32	84	90.3	16	4	US-10-209-421-29	Sequence 29, Appl
33	84	90.3	16	4	US-09-512-260A-5	Sequence 5, Appl
34	84	90.3	16	4	US-09-937-837-21	Sequence 21, Appl
35	84	90.3	16	4	US-10-009-049-6	Sequence 6, Appl
36	84	90.3	16	4	US-09-959-873B-10	Sequence 10, Appl
37	84	90.3	16	4	US-09-150-623-9	Sequence 9, Appl
38	84	90.3	16	4	US-09-748-063-3	Sequence 3, Appl
39	84	90.3	16	4	US-10-031-505-1	Sequence 1, Appl
40	84	90.3	16	4	US-10-144-549-1	Sequence 1, Appl
41	84	90.3	17	4	US-09-346-847-17	Sequence 17, Appl
42	84	90.3	17	4	US-09-346-847-20	Sequence 20, Appl
43	84	90.3	17	4	US-09-346-847-22	Sequence 22, Appl
44	84	90.3	17	4	US-09-346-847-27	Sequence 27, Appl
45	84	90.3	17	4	US-09-648-400A-30	Sequence 30, Appl

## ALIGNMENTS

RESULT 1

US-08-928-958-7

; Sequence 7, Application US/08928958

; Patent No. 5877282

; GENERAL INFORMATION:

; APPLICANT: NADLER, STEVEN G.

; APPLICANT: CLEAVELAND, JEFFREY S.

; APPLICANT: BLAKE, JAMES

; APPLICANT: HAFAR, OMAR K.

; TITLE OF INVENTION: PEPTIDE INHIBITORS OF NUCLEAR PROTEIN

; TITLE OF INVENTION: TRANSLLOCATION HAVING NUCLEAR LOCALIZATION SEQUENCES AND

; TITLE OF INVENTION: METHODS OF USE THEREOF

; NUMBER OF SEQUENCES: 24

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: ROBINS & ASSOCIATES

; STREET: 90 MIDDLEFIELD ROAD, SUITE 200

; CITY: MENLO PARK

; STATE: CA

; COUNTRY: USA

; ZIP: 94025

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/928,958

; FILING DATE: 12-SEP-1997

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/026978

; FILING DATE: 20-SEP-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: ROBINS, ROBERTA L.

; REGISTRATION NUMBER: 33,208

; REFERENCE/DOCKET NUMBER: 5998-0019

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (650) 325-7812

; TELEFAX: (650) 325-7823

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 16 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-928-958-7

Query Match 90.3%; Score 84; DB 2; Length 16;  
Best Local Similarity 93.8%; Pred. No. 3.5e-06;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RQIKWQNRRMKWFK 16  
Db 1 RQIKWQNRRMKWKK 16

## RESULT 2

US-08-810-540-3  
; Sequence 3, Application US/08810540  
; Patent No. 5929042  
; GENERAL INFORMATION:  
; APPLICANT: Troy, Carol M.  
; APPLICANT: Shelanski, Michael L.  
; TITLE OF INVENTION: ANTISENSE COMPOUNDS WHICH PREVENT CELL  
; TITLE OF INVENTION: DEATH AND USES THEREOF  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper & Dunham, LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10036

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/810,540  
; FILING DATE: 03-MAR-1997

CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White Esq., John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 0575/51247  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-278-0400  
; TELEFAX: 212-391-0526

INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide

US-08-810-540-3

Query Match 90.3%; Score 84; DB 2; Length 16;  
Best Local Similarity 93.8%; Pred. No. 3.5e-06;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RQIKWQNRRMKWFK 16  
Db 1 RQIKWQNRRMKWKK 16

## RESULT 3

US-08-810-540-6  
; Sequence 6, Application US/08810540  
; Patent No. 5929042  
; GENERAL INFORMATION:  
; APPLICANT: Troy, Carol M.  
; APPLICANT: Shelanski, Michael L.  
; TITLE OF INVENTION: ANTISENSE COMPOUNDS WHICH PREVENT CELL  
; TITLE OF INVENTION: DEATH AND USES THEREOF  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper & Dunham, LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: NY

COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/810,540  
; FILING DATE: 03-MAR-1997  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White Esq., John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 0575/51247  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-278-0400  
; TELEFAX: 212-391-0526

INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-810-540-6

Query Match 90.3%; Score 84; DB 2; Length 16;  
Best Local Similarity 93.8%; Pred. No. 3.5e-06;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RQIKWQNRRMKWFK 16  
Db 1 RQIKWQNRRMKWKK 16

## RESULT 4

US-09-072-429-7  
; Sequence 7, Application US/09072429  
; Patent No. 5962415  
; GENERAL INFORMATION:

APPLICANT: Nadler, Steven G.  
; TITLE OF INVENTION: COMPOSITIONS COMPRISING A PEPTIDE  
; TITLE OF INVENTION: INHIBITOR OF NUCLEAR PROTEIN TRANSLOCATION AND AN  
; TITLE OF INVENTION: IMMUNOSUPPRESSANT AND METHODS OF USE THEREOF  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Bristol-Myers Squibb Company  
; STREET: P.O. Box 4000  
; CITY: Princeton  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 08543-4000

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/072,429  
; FILING DATE: 04-MAY-1998  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Klein, Christopher A.  
; REGISTRATION NUMBER: 34,363  
; REFERENCE/DOCKET NUMBER: ON0141b  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (609) 252-3714  
; TELEFAX: (609) 252-4526

INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 amino acids  
; TYPE: amino acid



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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-072-429-7

Query Match          90.3%; Score 84; DB 2; Length 16;
Best Local Similarity 93.8%; Pred. No. 3.5e-06;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RQIKWQNRRMKWFK 16
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Db 1 RQIKWQNRRMKWKK 16

RESULT 5
US-08-964-302A-6
; Sequence 6, Application US/08964302A
; Patent No. 6015787
; GENERAL INFORMATION:
; APPLICANT: Potter, David A.
; APPLICANT: Skolnik, Paul R.
; TITLE OF INVENTION: CELL-PERMEABLE PROTEIN INHIBITORS OF CALPAIN
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Fast-SEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/964.302A
; FILING DATE: 04-NOV-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 00398/126001
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-964-302A-6

Query Match          90.3%; Score 84; DB 3; Length 16;
Best Local Similarity 93.8%; Pred. No. 3.5e-06;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RQIKWQNRRMKWFK 16
   |||||
Db 1 RQIKWQNRRMKWKK 16

RESULT 6
US-09-116-294-4
; Sequence 4, Application US/09116294
; Patent No. 6025140
; GENERAL INFORMATION:
; APPLICANT: Langel, Ulo
; APPLICANT: Bartfai, Tamas
; APPLICANT: Pooga, Margus
; APPLICANT: Valkna, Andres
; APPLICANT: Saar, Kulliki

; APPLICANT: Hallbrink, Mattias
; TITLE OF INVENTION: Conjugated Constructs of Peptides and
; FILE REFERENCE: 4394
; CURRENT APPLICATION NUMBER: US/09/116.294
; CURRENT FILING DATE: 1998-07-16
; EARLIER APPLICATION NUMBER: 60/052.678
; EARLIER FILING DATE: 1997-07-24
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 16
; TYPE: PPT
; ORGANISM: drosophila
US-09-116-294-4

Query Match          90.3%; Score 84; DB 3; Length 16;
Best Local Similarity 93.8%; Pred. No. 3.5e-06;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RQIKWQNRRMKWFK 16
   |||||
Db 1 RQIKWQNRRMKWKK 16

RESULT 7
US-08-964-614A-4
; Sequence 4, Application US/08964614A
; Patent No. 6057104
; GENERAL INFORMATION:
; APPLICANT: Hasty, Paul
; TITLE OF INVENTION: DISRUPTION OF THE MAMMALIAN
; TITLE OF INVENTION: Rad51 PROTEIN AND DISRUPTION OF PROTEINS THAT ASSOCIATE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds, LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: Fast-SEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/964.614A
; FILING DATE: 05-NOV-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/758,280
; FILING DATE: 05-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 8535-0019-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-964-614A-4

Query Match          90.3%; Score 84; DB 3; Length 16;
Best Local Similarity 93.8%; Pred. No. 3.5e-06;
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Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RQIKWQNRRMKWPK 16  
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Db 1 RQIKWQNRRMKWPK 16

RESULT 8  
US-08-849-486-1  
; Sequence 1, Application US/08849486  
; Patent No. 6080724  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: PEPTIDES WHICH CAN BE USED AS VECTORS  
; TITLE OF INVENTION: FOR THE INTRACELLULAR ADDRESSING OF ACTIVE MOLECULES  
; NUMBER OF SEQUENCES: 10  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/849,486  
; FILING DATE:  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 95 11714  
; FILING DATE: 05-OCT-1995  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-849-486-1

Query Match 90.3%; Score 84; DB 3; Length 16;  
Best Local Similarity 93.8%; Pred. No. 3.5e-06;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RQIKWQNRRMKWPK 16  
| | | | | | | | | | | | | | | | | |  
Db 1 RQIKWQNRRMKWPK 16

RESULT 9  
US-08-849-486-4  
; Sequence 4, Application US/08849486  
; Patent No. 6080724  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: PEPTIDES WHICH CAN BE USED AS VECTORS  
; TITLE OF INVENTION: FOR THE INTRACELLULAR ADDRESSING OF ACTIVE MOLECULES  
; NUMBER OF SEQUENCES: 10  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/849,486  
; FILING DATE:  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 95 11714  
; FILING DATE: 05-OCT-1995  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear

; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 1..16  
; OTHER INFORMATION: /product= "amino acids of the D series"  
US-08-849-486-4

Query Match 90.3%; Score 84; DB 3; Length 16;  
Best Local Similarity 93.8%; Pred. No. 3.5e-06;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RQIKWQNRRMKWPK 16  
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Db 1 RQIKWQNRRMKWPK 16

RESULT 10  
US-09-208-966-54  
; Sequence 54, Application US/09208966  
; Patent No. 6221355  
; GENERAL INFORMATION:  
; APPLICANT: Dowdy, Steven F.  
; TITLE OF INVENTION: ANTI-PATHOGEN SYSTEM AND METHODS OF USE THEREOF  
; FILE REFERENCE: 48881/1742  
; CURRENT APPLICATION NUMBER: US/09/208,966  
; CURRENT FILING DATE: 1998-12-10  
; EARLIER APPLICATION NUMBER: 60/082,402  
; EARLIER FILING DATE: 1998-04-20  
; EARLIER APPLICATION NUMBER: 60/069,012  
; EARLIER FILING DATE: 1997-12-10  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 54  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: human  
US-09-208-966-54

Query Match 90.3%; Score 84; DB 3; Length 16;  
Best Local Similarity 93.8%; Pred. No. 3.5e-06;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RQIKWQNRRMKWPK 16  
| | | | | | | | | | | | | | | | | |  
Db 1 RQIKWQNRRMKWPK 16

RESULT 11  
US-09-308-935-8  
; Sequence 8, Application US/09308935  
; Patent No. 6268334  
; GENERAL INFORMATION:  
; APPLICANT: La Thangue, Nicholas B  
; APPLICANT: Bandara, Lasantha R  
; TITLE OF INVENTION: Peptide antagonists of DP transcription factors  
; FILE REFERENCE: 620-67  
; CURRENT APPLICATION NUMBER: US/09/308,935  
; CURRENT FILING DATE: 1999-05-27  
; EARLIER APPLICATION NUMBER: PCT/GB97/03506  
; EARLIER FILING DATE: 1997-12-22  
; EARLIER APPLICATION NUMBER: GB 9626589.7  
; EARLIER FILING DATE: 1996-12-20  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 8  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Drosophila melanogaster  
US-09-308-935-8

Query Match 90.3%; Score 84; DB 3; Length 16;  
Best Local Similarity 93.8%; Pred. No. 3.5e-06;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 RQIKWQNRRMKWFK 16
Db 1 RQIKWQNRRMKWKK 16

RESULT 12
US-09-441-416A-6
; Sequence 6, Application US/09441416A
; Patent No. 6294518
; GENERAL INFORMATION:
; APPLICANT: Potter, David A.
; APPLICANT: Skolnik, Paul R.
; TITLE OF INVENTION: CELL-PERMEABLE PROTEIN INHIBITORS OF
; FILE REFERENCE: 00398-140001
; CURRENT APPLICATION NUMBER: US/09/441,416A
; CURRENT FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: US 08/964,302
; PRIOR FILING DATE: 1997-11-04
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-441-416A-6

Query Match 90.3%; Score 84; DB 3; Length 16;
Best Local Similarity 93.8%; Pred. No. 3.5e-06;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RQIKWQNRRMKWFK 16
Db 1 RQIKWQNRRMKWKK 16

RESULT 13
US-09-296-089-33
; Sequence 33, Application US/09296089
; Patent No. 6303576
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Byers, Stephen
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; FILE REFERENCE: 100086.411
; CURRENT APPLICATION NUMBER: US/09/296,089
; CURRENT FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 33
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-296-089-33

Query Match 90.3%; Score 84; DB 3; Length 16;
Best Local Similarity 93.8%; Pred. No. 3.5e-06;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RQIKWQNRRMKWFK 16
Db 1 RQIKWQNRRMKWKK 16

RESULT 14
US-09-419-826-35
; Sequence 35, Application US/09419826
; Patent No. 6306832
; GENERAL INFORMATION:
; APPLICANT:
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; TITLE OF INVENTION: PEPTIDE ANTIESTROGEN COMPOSITIONS AND METHODS
; TITLE OF INVENTION: FOR TREATING BREAST CANCER
; NUMBER OF SEQUENCES: 39
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/419,826
; FILING DATE: 14-OCT-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US98/07711
; FILING DATE: 14-APR-1998
; APPLICATION NUMBER: US 60/043,545
; FILING DATE: 14-APR-1997
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-09-419-826-35
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Query Match 90.3%; Score 84; DB 3; Length 16;  
Best Local Similarity 93.8%; Pred. No. 3.5e-06;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RQIKWQNRRMKWFK 16  
Db 1 RQIKWQNRRMKWKK 16

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RESULT 15
US-09-302-305C-10
; Sequence 10, Application US/09302305C
; Patent No. 6350572
; GENERAL INFORMATION:
; APPLICANT: Bernards, Rene
; APPLICANT: Zwijssen, Renate
; TITLE OF INVENTION: Interaction Between Cyclin D1 and Steroid Receptor
; TITLE OF INVENTION: Co-Activators and Uses Thereof in Assays
; FILE REFERENCE: 4238/80713
; CURRENT APPLICATION NUMBER: US/09/302,305C
; CURRENT FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: PCT/GB99/00440
; PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 10
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(16)
; OTHER INFORMATION: Translocation peptide derived from antennapedia
; OTHER INFORMATION: homeodomain protein
US-09-302-305C-10
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Query Match 90.3%; Score 84; DB 3; Length 16;  
Best Local Similarity 93.8%; Pred. No. 3.5e-06;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RQIKWQNRRMKWFK 16  
Db 1 RQIKWQNRRMKWKK 16

Search completed: March 31, 2005, 00:32:41  
Job time : 5.2 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 31, 2005, 00:25:06 ; Search time 7.69231 Seconds  
(without alignments)  
688.690 Million cell updates/sec

Title: US-10-049-822A-13

Perfect score: 93

Sequence: 1 RQIKWIFQNRMKWK 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1407402 seqs, 331100923 residues

Total number of hits satisfying chosen parameters: 1407402

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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18: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*  
19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*  
20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	85	91.4	17	9	US-09-854-204-34
2	84	90.3	16	8	US-08-610-220A-9
3	84	90.3	16	9	US-09-748-063-3
4	84	90.3	16	9	US-09-214-371-43
5	84	90.3	16	9	US-09-779-791A-3
6	84	90.3	16	9	US-09-780-070-38
7	84	90.3	16	9	US-09-150-623-9
8	84	90.3	16	9	US-09-731-023A-10
9	84	90.3	16	9	US-09-854-204-1
10	84	90.3	16	9	US-09-900-147-8
11	84	90.3	16	9	US-09-792-480-29
12	84	90.3	16	9	US-09-785-802A-2
13	84	90.3	16	9	US-09-785-802A-5

Sequence 32, Appl  
Sequence 10, Appl  
Sequence 3, Appl  
Sequence 6, Appl  
Sequence 6, Appl  
Sequence 54, Appl  
Sequence 4, Appl  
Sequence 1, Appl  
Sequence 2, Appl  
Sequence 3, Appl  
Sequence 12, Appl  
Sequence 3, Appl  
Sequence 29, Appl  
Sequence 2, Appl  
Sequence 3, Appl  
Sequence 3, Appl  
Sequence 10, Appl  
Sequence 1, Appl  
Sequence 25, Appl  
Sequence 21, Appl  
Sequence 14, Appl  
Sequence 11, Appl  
Sequence 14, Appl  
Sequence 1, Appl  
Sequence 10, Appl  
Sequence 2, Appl  
Sequence 34, Application US/09854204  
Patent No. US20020098236A1  
GENERAL INFORMATION:  
APPLICANT: Fischer, Peter Martin  
APPLICANT: Zhelev, Nikolai  
TITLE OF INVENTION: Transport Vectors  
FILE REFERENCE: CCI-010  
CURRENT APPLICATION NUMBER: US/09/854,204  
CURRENT FILING DATE: 2001-05-11  
PRIOR APPLICATION NUMBER: 09/438,460  
PRIOR FILING DATE: 1999-11-12  
PRIOR APPLICATION NUMBER: GB 9825000.4  
PRIOR FILING DATE: 1998-11-13  
PRIOR APPLICATION NUMBER: GB 9825001.2  
PRIOR FILING DATE: 1998-11-13  
PRIOR APPLICATION NUMBER: GB 9902525.6  
PRIOR FILING DATE: 1999-02-04  
PRIOR APPLICATION NUMBER: GB 9902522.3  
PRIOR FILING DATE: 1999-02-04  
PRIOR APPLICATION NUMBER: GB 9914578.1  
PRIOR FILING DATE: 1999-06-22  
PRIOR APPLICATION NUMBER: PCT/GB99/03750  
PRIOR FILING DATE: 1999-11-11  
NUMBER OF SEQ ID NOS: 66  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 34  
LENGTH: 17  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: MOD\_RES  
LOCATION: (1)  
OTHER INFORMATION: bala  
NAME/KEY: MOD\_RES

#### ALIGNMENTS

RESULT 1  
US-09-854-204-34  
Sequence 34, Application US/09854204  
GENERAL INFORMATION:  
APPLICANT: Fischer, Peter Martin  
APPLICANT: Zhelev, Nikolai  
TITLE OF INVENTION: Transport Vectors  
FILE REFERENCE: CCI-010  
CURRENT APPLICATION NUMBER: US/09/854,204  
CURRENT FILING DATE: 2001-05-11  
PRIOR APPLICATION NUMBER: 09/438,460  
PRIOR FILING DATE: 1999-11-12  
PRIOR APPLICATION NUMBER: GB 9825000.4  
PRIOR FILING DATE: 1998-11-13  
PRIOR APPLICATION NUMBER: GB 9825001.2  
PRIOR FILING DATE: 1998-11-13  
PRIOR APPLICATION NUMBER: GB 9902525.6  
PRIOR FILING DATE: 1999-02-04  
PRIOR APPLICATION NUMBER: GB 9902522.3  
PRIOR FILING DATE: 1999-02-04  
PRIOR APPLICATION NUMBER: GB 9914578.1  
PRIOR FILING DATE: 1999-06-22  
PRIOR APPLICATION NUMBER: PCT/GB99/03750  
PRIOR FILING DATE: 1999-11-11  
NUMBER OF SEQ ID NOS: 66  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 34  
LENGTH: 17  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: MOD\_RES  
LOCATION: (1)  
OTHER INFORMATION: bala  
NAME/KEY: MOD\_RES

; LOCATION: (17)  
 ; OTHER INFORMATION: AMIDATION  
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 ; OTHER INFORMATION: sequence  
 US-09-854-204-34

Query Match 91.4%; Score 85; DB 9; Length 17;  
 Best Local Similarity 93.8%; Pred. No. 2.6e-05;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RQIKWFOQRMMKWK 16  
 Db 2 RQIKWFOQRMMKWK 17

RESULT 2  
 US-08-610-220A-9  
 ; Sequence 9, Application US/08610220A  
 ; Publication No. US20030099638A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Troy Carol M.  
 ; TITLE OF INVENTION: COMPOUNDS WHICH PREVENT NEURONAL CELL  
 ; TITLE OF INVENTION: DEATH AND USES THEREOF  
 ; NUMBER OF SEQUENCES: 11  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Cooper & Dunham LLP  
 ; STREET: 1185 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: U.S.A.  
 ; ZIP: 10036  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/610,220A  
 ; FILING DATE: MAR-04-1996  
 ; CLASSIFICATION: 424  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: White, John P.  
 ; REGISTRATION NUMBER: 28,678  
 ; REFERENCE/DOCKET NUMBER: 48332/JPW/JML  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 212-278-0400  
 ; TELEFAX: 212-391-0525  
 ; INFORMATION FOR SEQ ID NO: 9:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 16 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 US-08-610-220A-9

Query Match 90.3%; Score 84; DB 8; Length 16;  
 Best Local Similarity 93.8%; Pred. No. 3.4e-05;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RQIKWFOQRMMKWK 16  
 Db 1 RQIKWFOQRMMKWK 16

RESULT 3  
 US-09-748-063-3  
 ; Sequence 3, Application US/09748063  
 ; Publication No. US20010008758A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: McHale, Anthony P.  
 ; APPLICANT: Craig, Roger  
 ; APPLICANT: Haro, Anna Maria Rollan

; TITLE OF INVENTION: Delivery of an Agent  
 ; FILE REFERENCE: 11067/1060  
 ; CURRENT APPLICATION NUMBER: US/09/748,063  
 ; CURRENT FILING DATE: 2000-12-22  
 ; PRIOR APPLICATION NUMBER: PCT/GB00/02848  
 ; PRIOR FILING DATE: 2000-07-24  
 ; PRIOR APPLICATION NUMBER: US 60/146,556  
 ; PRIOR FILING DATE: 2000-07-30  
 ; PRIOR APPLICATION NUMBER: GB 9917416.1  
 ; PRIOR FILING DATE: 1999-07-23  
 ; NUMBER OF SEQ ID NOS: 3  
 ; SOFTWARE: Patent in version 3.1  
 ; SEQ ID NO 3  
 ; LENGTH: 16  
 ; TYPE: PRT  
 ; ORGANISM: Drosophila sp.  
 US-09-748-063-3  
 Query Match 90.3%; Score 84; DB 9; Length 16;  
 Best Local Similarity 93.8%; Pred. No. 3.4e-05;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 RQIKWFOQRMMKWK 16  
 Db 1 RQIKWFOQRMMKWK 16  
 RESULT 4  
 US-09-214-371-43  
 ; Sequence 43, Application US/09214371B  
 ; Patent No. US20010018511A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lane, David  
 ; APPLICANT: Bottger, Volker  
 ; APPLICANT: Bottger, Angelica  
 ; APPLICANT: Pickles, Stephen  
 ; APPLICANT: Chene, Patrick  
 ; APPLICANT: Hochkeppel, Heinz-Kurt  
 ; APPLICANT: Garcia-Echeverria, Carlos  
 ; APPLICANT: Furet, Pascal  
 ; TITLE OF INVENTION: Inhibitors of the Interaction of P53 and MDM2  
 ; FILE REFERENCE: 4-20937/A/PCT  
 ; CURRENT APPLICATION NUMBER: US/09/214,371B  
 ; CURRENT FILING DATE: 1999-03-26  
 ; PRIOR APPLICATION NUMBER: PCT/EP97/03549  
 ; PRIOR FILING DATE: 1997-07-04  
 ; NUMBER OF SEQ ID NOS: 83  
 ; SOFTWARE: Patent in Ver. 2.0  
 ; SEQ ID NO 43  
 ; LENGTH: 16  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence:peptide  
 US-09-214-371-43  
 Query Match 90.3%; Score 84; DB 9; Length 16;  
 Best Local Similarity 93.8%; Pred. No. 3.4e-05;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RQIKWFOQRMMKWK 16  
 Db 1 RQIKWFOQRMMKWK 16  
 RESULT 5  
 US-09-779-791A-3  
 ; Sequence 3, Application US/09779791A  
 ; Publication No. US2001004417A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Mirus Corporation  
 ; APPLICANT: Wolff, Jon A  
 ; APPLICANT: Monahan, Sean D

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; APPLICANT: Budker, Vladimir G
; APPLICANT: Slatum, Paul M
; APPLICANT: Rozema, David B
; TITLE OF INVENTION: A Compound Containing a Labile Disulfide Bond
; FILE REFERENCE: Mirus.006.03
; CURRENT APPLICATION NUMBER: US/09/779,791A
; CURRENT FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: 09/312,351
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-779-791A-3

Query Match          90.3%; Score 84; DB 9; Length 16;
Best Local Similarity 93.8%; Pred. No. 3.4e-05;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RQIKWQNRRMKWFK 16
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Db 1 RQIKWQNRRMKWKK 16

RESULT 6
US-09-780-070-38
; Sequence 38, Application US/09780070
; Patent No. US2002009752A1
; GENERAL INFORMATION:
; APPLICANT: Burke, James
; APPLICANT: Strittmatter, Warren
; APPLICANT: Nagai, Yoshitaka
; TITLE OF INVENTION: COMPOUNDS THAT SELECTIVELY BIND TO EXPANDED POLYGLUTAMINE REPEAT
; TITLE OF INVENTION: COMPOUNDS THAT SELECTIVELY BIND TO EXPANDED POLYGLUTAMINE REPEAT
; FILE REFERENCE: 5405.242
; CURRENT APPLICATION NUMBER: US/09/780,070
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/189,781
; PRIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 38
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-780-070-38

Query Match          90.3%; Score 84; DB 9; Length 16;
Best Local Similarity 93.8%; Pred. No. 3.4e-05;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RQIKWQNRRMKWFK 16
   |||||
Db 1 RQIKWQNRRMKWKK 16

RESULT 7
US-09-150-623-9
; Sequence 9, Application US/09150623
; Patent No. US2002004931A1
; GENERAL INFORMATION:
; APPLICANT: Troy, Carol M.
; TITLE OF INVENTION: COMPOUNDS WHICH PREVENT NEURONAL CELL
; TITLE OF INVENTION: DEATH AND USES THEREOF
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
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; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/150,623
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/610,220
; FILING DATE: MAR-04-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 48332/JPW/JML
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-391-0525
; TELEFAX: 212-278-0400
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-150-623-9

Query Match          90.3%; Score 84; DB 9; Length 16;
Best Local Similarity 93.8%; Pred. No. 3.4e-05;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RQIKWQNRRMKWFK 16
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Db 1 RQIKWQNRRMKWKK 16

RESULT 8
US-09-731-023A-10
; Sequence 10, Application US/09731023A
; Patent No. US2002007283A1
; GENERAL INFORMATION:
; APPLICANT: Sessa, William
; TITLE OF INVENTION: Caveolin Peptides and Their Use as Therapeutics
; FILE REFERENCE: 44574-5076-US
; CURRENT APPLICATION NUMBER: US/09/731,023A
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/231,327
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; NAME/KEY: DOMAIN
; LOCATION: (1)...(16)
; OTHER INFORMATION: Homeodomain, internalization sequence
US-09-731-023A-10

Query Match          90.3%; Score 84; DB 9; Length 16;
Best Local Similarity 93.8%; Pred. No. 3.4e-05;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RQIKWQNRRMKWFK 16
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Db 1 RQIKWQNRRMKWKK 16

RESULT 9
US-09-854-204-1
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; Sequence 1, Application US/09854204  
; Patent No. US20020098236A1  
; GENERAL INFORMATION:  
; APPLICANT: Fischer, Peter Martin  
; APPLICANT: Zhelev, Nikolai  
; TITLE OF INVENTION: Transport Vectors  
; FILE REFERENCE: CCI-010  
; CURRENT APPLICATION NUMBER: US/09/854,204  
; PRIOR FILING DATE: 2001-05-11  
; PRIOR APPLICATION NUMBER: 09/438,460  
; PRIOR FILING DATE: 1999-11-12  
; PRIOR APPLICATION NUMBER: GB 9825000.4  
; PRIOR FILING DATE: 1998-11-13  
; PRIOR APPLICATION NUMBER: GB 9825001.2  
; PRIOR FILING DATE: 1998-11-13  
; PRIOR APPLICATION NUMBER: GB 9902525.6  
; PRIOR FILING DATE: 1999-02-04  
; PRIOR APPLICATION NUMBER: GB 9902522.3  
; PRIOR FILING DATE: 1999-02-04  
; PRIOR APPLICATION NUMBER: GB 9914578.1  
; PRIOR FILING DATE: 1999-06-22  
; PRIOR APPLICATION NUMBER: PCT/GB99/03750  
; PRIOR FILING DATE: 1999-11-11  
; NUMBER OF SEQ ID NOS: 66  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Drosophila melanogaster  
US-09-854-204-1

Query Match 90.3%; Score 84; DB 9; Length 16;  
Best Local Similarity 93.8%; Pred. No. 3.4e-05;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RQIKWFFQNRRMKWFK 16  
| | | | | | | | | | | | | | | |  
Db 1 RQIKWFFQNRRMKWKK 16

RESULT 10  
US-09-900-147-8  
; Sequence 8, Application US/09900147  
; Patent No. US20020103121A1  
; GENERAL INFORMATION:  
; APPLICANT: La Thangue, Nicholas B  
; APPLICANT: Bandara, Lasantha R  
; TITLE OF INVENTION: Peptide antagonists of DP transcription factors  
; FILE REFERENCE: 620-67  
; CURRENT APPLICATION NUMBER: US/09/900,147  
; PRIOR FILING DATE: 2001-07-09  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/308,935  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-05-27  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: GB 9626589.7  
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-12-20  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 8  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Drosophila melanogaster  
US-09-900-147-8

Query Match 90.3%; Score 84; DB 9; Length 16;  
Best Local Similarity 93.8%; Pred. No. 3.4e-05;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RQIKWFFQNRRMKWFK 16  
| | | | | | | | | | | | | | | |  
Db 1 RQIKWFFQNRRMKWKK 16

RESULT 11

US-09-792-480-29  
; Sequence 29, Application US/09792480  
; Patent No. US20020127198A1  
; GENERAL INFORMATION:  
; APPLICANT: Rothbard, Jonathan B.  
; APPLICANT: Wender, Paul A.  
; APPLICANT: McGrane, P. Leo  
; APPLICANT: Sista, Lalitha V.S.  
; APPLICANT: Kirschberg, Thorsten A.  
; APPLICANT: CellGate, Inc.  
; TITLE OF INVENTION: Compositions and Methods for Enhancing Drug Delivery  
; FILE REFERENCE: 019801-000230US  
; CURRENT APPLICATION NUMBER: US/09/792,480  
; PRIOR FILING DATE: 2001-02-23  
; PRIOR APPLICATION NUMBER: US 09/648,400  
; PRIOR FILING DATE: 2000-08-24  
; PRIOR APPLICATION NUMBER: US 60/150,510  
; PRIOR FILING DATE: 1999-08-24  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 29  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:Antennapedia  
; OTHER INFORMATION: homeodomain, Antennapedia-43-58  
US-09-792-480-29

Query Match 90.3%; Score 84; DB 9; Length 16;  
Best Local Similarity 93.8%; Pred. No. 3.4e-05;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RQIKWFFQNRRMKWFK 16  
| | | | | | | | | | | | | | | |  
Db 1 RQIKWFFQNRRMKWKK 16

RESULT 12  
US-09-785-802A-2  
; Sequence 2, Application US/09785802A  
; Patent No. US20020151004A1  
; GENERAL INFORMATION:  
; APPLICANT: Craig, Roger  
; TITLE OF INVENTION: DELIVERY VEHICLES AND METHODS FOR USING THE SAME  
; FILE REFERENCE: 11067/2035  
; CURRENT APPLICATION NUMBER: US/09/785,802A  
; CURRENT FILING DATE: 2001-02-16  
; PRIOR APPLICATION NUMBER: US 09/748,06  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: US 09/748,789  
; PRIOR FILING DATE: 2000-12-22  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Membrane translocation sequence from Penetratin  
US-09-785-802A-2

Query Match 90.3%; Score 84; DB 9; Length 16;  
Best Local Similarity 93.8%; Pred. No. 3.4e-05;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RQIKWFFQNRRMKWFK 16  
| | | | | | | | | | | | | | | |  
Db 1 RQIKWFFQNRRMKWKK 16

RESULT 13



```
US-09-785-802A-5
; Sequence 5, Application US/09785802A
; Patent No. US20020151004A1
; GENERAL INFORMATION:
; APPLICANT: Craig, Roger
; TITLE OF INVENTION: DELIVERY VEHICLES AND METHODS FOR USING THE SAME
; FILE REFERENCE: 11067/2035
; CURRENT APPLICATION NUMBER: US/09/785,802A
; CURRENT FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 09/748,06
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/748,789
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 5
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-785-802A-5
Query Match          90.3%; Score 84; DB 9; Length 16;
Best Local Similarity 93.8%; Pred. No. 3.4e-05;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RQIKWQNRRMKWFK 16
   |||||
Db 1 RQIKWQNRRMKWKK 16

RESULT 14
US-09-902-432-32
; Sequence 32, Application US/09902432
; Patent No. US2002016002A1
; GENERAL INFORMATION:
; APPLICANT: Irwin H. Gelman
; APPLICANT: Susan G. Jaken
; TITLE OF INVENTION: TUMOR SUPPRESSOR GENE
; FILE REFERENCE: A30558-A-FWC-A 070156.0597
; CURRENT APPLICATION NUMBER: US/09/902,432
; CURRENT FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: 08/978,277
; PRIOR FILING DATE: 1997-11-25
; PRIOR APPLICATION NUMBER: 08/665,401
; PRIOR FILING DATE: 1996-06-18
; PRIOR APPLICATION NUMBER: 08/635,121
; PRIOR FILING DATE: 1996-04-19
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Penetratin peptide
US-09-902-432-32
Query Match          90.3%; Score 84; DB 9; Length 16;
Best Local Similarity 93.8%; Pred. No. 3.4e-05;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RQIKWQNRRMKWFK 16
   |||||
Db 1 RQIKWQNRRMKWKK 16

RESULT 15
US-09-953-031A-10
; Sequence 10, Application US/09953031A
; Patent No. US2002017717A1
; GENERAL INFORMATION:
; APPLICANT: Bernards, Rene
; APPLICANT: Zwijssen, Renate
```

```
; TITLE OF INVENTION: Interaction Between Cyclin D1 and Steroid Receptor
; FILE REFERENCE: 4238/80713
; CURRENT APPLICATION NUMBER: US/09/953,031A
; CURRENT FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: US 09/302,305
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 10
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(16)
; OTHER INFORMATION: Translocation peptide derived from antennapedia
; OTHER INFORMATION: homeodomain protein
US-09-953-031A-10
Query Match          90.3%; Score 84; DB 9; Length 16;
Best Local Similarity 93.8%; Pred. No. 3.4e-05;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RQIKWQNRRMKWFK 16
   |||||
Db 1 RQIKWQNRRMKWKK 16

Search completed: March 31, 2005, 00:34:58
Job time : 9.69231 secs
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100

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 31, 2005, 00:22:11 ; Search time 2.09231 Seconds  
(without alignments)  
735.775 Million cell updates/sec

Title: US-10-049-822a-13

Perfect score: 93

Sequence: 1 RQIKWIFQNRMRKWK 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR.79.\*

2: PIR1.\*

3: PIR3.\*

4: PIR4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
1	84	90.3	33	2 S57235	antennapedia prote
2	84	90.3	42	2 I65241	homeotic protein H
3	84	90.3	45	2 PC1216	homeotic protein D
4	84	90.3	48	2 I51439	homeobox protein -
5	84	90.3	50	2 S10907	homeotic protein (
6	84	90.3	66	2 S15538	homeotic protein H
7	84	90.3	66	2 S15536	homeotic protein H
8	84	90.3	71	2 JC1161	homeotic protein 3
9	84	90.3	71	2 A60084	homeotic protein H
10	84	90.3	74	2 D34510	homeotic protein H
11	84	90.3	75	2 S58852	homeotic protein S
12	84	90.3	75	2 I51341	homeo box protein
13	84	90.3	76	2 C43559	homeo box protein R
14	84	90.3	78	2 I51342	homeo box protein
15	84	90.3	81	2 B29585	homeotic protein H
16	84	90.3	81	2 S47605	homeotic protein H
17	84	90.3	82	2 S08302	homeotic protein H
18	84	90.3	83	2 S50066	homeotic protein H
19	84	90.3	83	2 S47603	homeotic protein H
20	84	90.3	86	2 A34510	homeotic protein H
21	84	90.3	86	2 S08303	homeotic protein H
22	84	90.3	86	2 JT0489	homeotic protein Z
23	84	90.3	87	2 S00589	homeotic protein M
24	84	90.3	88	2 A03317	homeotic protein H
25	84	90.3	96	2 S08639	homeotic protein z
26	84	90.3	96	2 A05266	homeotic protein H
27	84	90.3	97	2 C27176	homeotic protein H
28	84	90.3	97	2 A24779	homeotic protein m
29	84	90.3	103	2 A32167	homeotic protein H

30	84	90.3	105	2 S47602	homeotic protein H
31	84	90.3	105	2 A27471	homeotic protein R
32	84	90.3	106	2 S36448	homeotic protein s
33	84	90.3	107	2 B61045	homeotic protein T
34	84	90.3	113	2 T10775	homeobox protein -
35	84	90.3	118	2 A24777	homeotic protein H
36	84	90.3	118	2 JT0273	homeotic protein H
37	84	90.3	118	2 B24777	homeotic protein M
38	84	90.3	119	2 A03314	homeotic protein m
39	84	90.3	138	2 S20087	homeotic protein b
40	84	90.3	148	2 PC4071	homeobox A5 protei
41	84	90.3	153	1 WJHU3C	homeotic protein H
42	84	90.3	153	1 WJMSX6	homeotic protein H
43	84	90.3	158	2 A27348	homeotic protein H
44	84	90.3	209	2 A43553	homeotic protein H
45	84	90.3	217	1 WJHU2C	homeotic protein H

#### ALIGNMENTS

##### RESULT 1

S57235

antennapedia protein (clone pl105) - fruit fly (Drosophila pseudoobscura) (fragment)  
C:Species: Drosophila pseudoobscura

C:Date: 10-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 16-Aug-2004

C:Accession: S57235

R:Randazzo, F.M.; Seeger, M.A.; Huss, C.A.; Sweeney, M.A.; Cecil, J.K.; Kaufman, T.C.  
Genetics 133, 319-330, 1993

A:Title: Structural changes in the antennapedia complex of Drosophila pseudoobscura.

A:Reference number: S57224

A:Accession: S57235

A:Molecule type: DNA

A:Residues: 1-33 <RAN>

A:Cross-references: EMBL:X77711

C:Genetics:

A:Gene: FlyBase:Antp

A:Cross-references: FlyBase:FBgn0012693

C:Superfamily: homeobox homology

C:Keywords: DNA binding; homeobox; nucleus; transcription regulation

F:1-22/Domain: homeobox homology (fragment) <HOX>

Query Match 90.3%; Score 84; DB 2; Length 33;

Best Local Similarity 93.8%; Pred. No. 3.1e-06;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RQIKWIFQNRMRKWK 16

Db 7 RQIKWIFQNRMRKWK 22

##### RESULT 2

I65241

homeotic protein Hox-A - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)

C:Date: 27-Feb-1997 #sequence\_revision 27-Feb-1997 #text\_change 16-Aug-2004

C:Accession: I65241

R:Sakoyama, Y.; Mizuta, I.; Ogasawara, N.; Yoshikawa, H.

Biochem. Genet. 32, 351-360, 1994

A:Title: Cloning of rat homeobox genes.

A:Reference number: 152340; MUID:95217128; PMID:7702549

A:Accession: I65241

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-42 <RES>

A:Cross-references: GB:S76290; NID:g913077

C:Genetics:

A:Gene: Hox-A; Hox-1

C:Superfamily: homeobox homology

C:Keywords: DNA binding; homeobox; nucleus; transcription regulation

F:1-40/Domain: homeobox homology (fragment) <HOX>

Query Match 90.3%; Score 84; DB 2; Length 42;

Best Local Similarity 93.8%; Pred. NO. 3.9e-06;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RQIKWQNRRMKWFK 16  
| | | | | | | | | | | | | | | | | | | | |  
Db 25 RQIKWQNRRMKWKK 40

RESULT 3  
PC1216  
homeotic protein DtlHx1 - planarian (*Dugesia tigrina*) (fragment)  
A:Species: *Dugesia tigrina*  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-2004  
C:Accession: PC1216  
R:Oliver, G.; Vispo, M.; Mailhos, A.; Martinez, C.; Sosa-Pineda, B.; Flietiz, W.; Ehrlich  
Gene 121, 337-342, 1992  
A:Title: Homeoboxes in flatworms.  
A:Reference number: JC1386; MUID:93077050; PMID:1359988  
A:Accession: PC1216  
A:Molecule type: DNA  
A:Residues: 1-45 <OLI>  
A:Cross-references: UNIPROT:P91714; EMBL:X66822  
C:Superfamily: homeobox homology  
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation  
F;1-45/Domain: homeobox homology (fragment) <HOX>

Query Match 90.3%; Score 84; DB 2; Length 45;  
Best Local Similarity 93.8%; Pred. NO. 4.1e-06;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RQIKWQNRRMKWFK 16  
| | | | | | | | | | | | | | | | | | | | |  
Db 30 RQIKWQNRRMKWKK 45

RESULT 4  
I51439  
homeobox protein - African clawed frog (fragment)  
C:Species: *Xenopus laevis* (African clawed frog)  
C:Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 16-Aug-2004  
C:Accession: I51439  
R:Leroy, P.; DeRobertis, E.M.  
Dev. Dyn. 194, 21-32, 1992  
A:Title: Effects of lithium chloride and retinoic acid on the expression of genes from t  
A:Reference number: I51439; MUID:93043517; PMID:1384809  
A:Accession: I51439  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-48 <LER>  
A:Cross-references: UNIPROT:P31256; GB:M91587; NID:G214257; PIDN:AAA49750.1; PID:G214258  
C:Genetics:  
A:Gene: Hox2.2  
C:Superfamily: homeobox homology  
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation  
F;1-27/Domain: homeobox homology (fragment) <HOX>

Query Match 90.3%; Score 84; DB 2; Length 48;  
Best Local Similarity 93.8%; Pred. NO. 4.4e-06;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RQIKWQNRRMKWFK 16  
| | | | | | | | | | | | | | | | | | | | |  
Db 12 RQIKWQNRRMKWKK 27

RESULT 5  
S10907  
homeotic protein (clone 11-2-1) - human (fragment)  
C:Species: *Homo sapiens* (man)  
C:Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 16-Aug-2004  
C:Accession: S10907  
R:Gilman, J.G.  
submitted to the EMBL Data Library, April 1990

A:Reference number: S10907  
A:Accession: S10907  
A:Molecule type: mRNA  
A:Residues: 1-50 <GIL>  
A:Cross-references: UNIPROT:Q14543; EMBL:X52402; NID:G32360; PIDN:CAA36647.1; PID:G32361  
C:Superfamily: homeobox homology  
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation  
F;1-40/Domain: homeobox homology (fragment) <HOX>

Query Match 90.3%; Score 84; DB 2; Length 50;  
Best Local Similarity 93.8%; Pred. NO. 4.6e-06;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RQIKWQNRRMKWFK 16  
| | | | | | | | | | | | | | | | | | | | |  
Db 25 RQIKWQNRRMKWKK 40

RESULT 6  
S15538  
homeotic protein Hox A6 - human (fragment)  
N:Alternate names: homeotic protein Hox 1B  
C:Species: *Homo sapiens* (man)  
C:Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 16-Aug-2004  
C:Accession: S15538  
R:Boncinelli, E.; Acampora, D.; Pannese, M.; d'Esposito, M.; Somma, R.; Gaudino, G.; Sto  
Genome 31, 745-756, 1989  
A:Title: Organization of human class I homeobox genes.  
A:Reference number: S15036; MUID:90215256; PMID:2576652  
A:Accession: S15538  
A:Status: not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 1-66 <BON>  
A:Cross-references: UNIPROT:P31267  
C:Genetics:  
A:Gene: GDB:H0XA6  
A:Cross-references: GDB:I20648; OMIM:142951  
A:Map position: 7p15.3-7p15.3  
C:Superfamily: homeobox homology  
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation  
F;2-58/Domain: homeobox homology <HOX>

Query Match 90.3%; Score 84; DB 2; Length 66;  
Best Local Similarity 93.8%; Pred. NO. 6e-06;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RQIKWQNRRMKWFK 16  
| | | | | | | | | | | | | | | | | | | | |  
Db 43 RQIKWQNRRMKWKK 58

RESULT 7  
S15536  
homeotic protein Hox A7 - human (fragment)  
N:Alternate names: homeotic protein Hox 1A  
C:Species: *Homo sapiens* (man)  
C:Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 16-Aug-2004  
C:Accession: S15536  
R:Boncinelli, E.; Acampora, D.; Pannese, M.; d'Esposito, M.; Somma, R.; Gaudino, G.; Sto  
Genome 31, 745-756, 1989  
A:Title: Organization of human class I homeobox genes.  
A:Reference number: S15036; MUID:90215256; PMID:2576652  
A:Accession: S15536  
A:Status: not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 1-66 <BON>  
A:Cross-references: UNIPROT:P31268  
C:Genetics:  
A:Gene: GDB:H0XA7  
A:Cross-references: GDB:I20647; OMIM:142950  
A:Map position: 7p15.3-7p15.3  
C:Superfamily: homeobox homology  
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation

F;2-58/Domain: homeobox homology <HOX>

Query Match 90.3%; Score 84; DB 2; Length 66;  
Best Local Similarity 93.8%; Pred. No. 6e-06;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RQIKWQNRRMKWFK 16  
|||  
Db 43 RQIKWQNRRMKWKK 58

# RESULT 8

JC1161  
homeotic protein 3.4 - eastern newt (fragment)  
C;Species: Notophthalmus viridescens, Triturus viridescens (eastern newt)  
C;Date: 09-Oct-1992 #sequence\_revision 09-Oct-1992 #text\_change 16-Aug-2004  
C;Accession: JC1161  
R;Belleville, S.; Beauchemin, M.; Tremblay, M.; Noisieux, N.; Savard, P.  
Gene 114, 179-186, 1992  
A;Title: Homeobox-containing genes in the newt are organized in clusters similar to other  
A;Reference number: JC1161; MUID:92290273; PMID:1351019  
A;Accession: JC1161  
A;Molecule type: DNA  
A;Residues: 1-71 <BEL>  
A;Cross-references: UNIPROT:P31262; GB:M84001  
C;Genetics:  
A;Gene: NvHox-3.4  
C;Superfamily: homeobox homology  
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation  
F;5-61/Domain: homeobox homology <HOX>

Query Match 90.3%; Score 84; DB 2; Length 71;  
Best Local Similarity 93.8%; Pred. No. 6.4e-06;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RQIKWQNRRMKWFK 16  
|||  
Db 46 RQIKWQNRRMKWKK 61

# RESULT 9

A60084  
homeotic protein Hox 3.4 - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 20-Feb-1993 #sequence\_revision 20-Feb-1993 #text\_change 09-Jul-2004  
C;Accession: A60084  
R;Gaut, S.J.; Coletta, P.L.; Pravtcheva, D.; Sharpe, P.T.  
Development 109, 329-339, 1990  
A;Title: Mouse Hox-3.4: homeobox sequence and embryonic expression patterns compared with  
A;Reference number: A60084; MUID:90382249; PMID:1976088  
A;Accession: A60084  
A;Status: not compared with conceptual translation  
A;Molecule type: DNA  
A;Residues: 1-71 <GAU>  
A;Cross-references: UNIPROT:P32043  
C;Genetics:  
A;Map position: 15  
C;Superfamily: unassigned homeobox proteins; homeobox homology  
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation  
F;5-61/Domain: homeobox homology <HOX>

Query Match 90.3%; Score 84; DB 2; Length 71;  
Best Local Similarity 93.8%; Pred. No. 6.4e-06;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RQIKWQNRRMKWFK 16  
|||  
Db 46 RQIKWQNRRMKWKK 61

# RESULT 10

D34510  
homeotic protein H90 - honeybee (fragment)

C;Species: Apis mellifera (honeybee)  
C;Date: 22-Jun-1990 #sequence\_revision 09-Oct-1992 #text\_change 16-Aug-2004  
C;Accession: D34510  
R;Walldorf, U.; Fleig, R.; Gehring, W.J.  
Proc. Natl. Acad. Sci. U.S.A. 86, 9971-9975, 1989  
A;Title: Comparison of homeobox-containing genes of the honeybee and Drosophila.  
A;Reference number: A34510; MUID:9009384; PMID:2574865  
A;Accession: D34510  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-74 <WAL>  
A;Cross-references: UNIPROT:P15860; GB:M29493; NID:g155675; PIDN:AAA27728.1; PID:g155676  
A;Note: the authors mistranslated the codons for residues 68-74  
C;Superfamily: homeobox homology  
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation  
F;9-65/Domain: homeobox homology <HOX>

Query Match 90.3%; Score 84; DB 2; Length 74;  
Best Local Similarity 93.8%; Pred. No. 6.7e-06;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RQIKWQNRRMKWFK 16  
|||  
Db 50 RQIKWQNRRMKWKK 65

# RESULT 11

S58852  
homeotic protein Scr homolog - Junonia coenia (fragment)  
N;Alternate names: sex combs reduced homeodomain protein  
C;Species: Junonia coenia  
C;Date: 19-Mar-1997 #sequence\_revision 29-Aug-1997 #text\_change 16-Aug-2004  
C;Accession: S58852  
R;Warren, R.W.; Nagy, L.; Sealeg, J.; Gates, J.; Carroll, S.  
Nature 372, 458-461, 1994  
A;Title: Evolution of homeotic gene regulation and function in flies and butterflies.  
A;Reference number: S58850; MUID:95075456; PMID:7840822  
A;Accession: S58852  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-75 <WAR>  
A;Cross-references: UNIPROT:Q25209; EMBL:L42136; NID:g806495; PIDN:AAA68462.1; PID:g8064  
C;Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1995  
C;Superfamily: homeobox homology  
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation  
F;1-40/Domain: homeobox homology (fragment) <HOK>

Query Match 90.3%; Score 84; DB 2; Length 75;  
Best Local Similarity 93.8%; Pred. No. 6.8e-06;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RQIKWQNRRMKWFK 16  
|||  
Db 25 RQIKWQNRRMKWKK 40

# RESULT 12

I51341  
homeo box protein - Atlantic salmon (fragment)  
C;Species: Salmo salar (Atlantic salmon)  
C;Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 16-Aug-2004  
C;Accession: I51341  
R;Fjose, A.; Molven, A.; Eiken, H.G.  
Gene 62, 141-152, 1988  
A;Title: Molecular cloning and characterization of homeobox-containing genes from Atlantic  
A;Reference number: I51341; MUID:88226009; PMID:2897318  
A;Accession: I51341  
A;Status: preliminary; translated from GB/EMBL/DBDJ  
A;Molecule type: DNA  
A;Residues: 1-75 <FJO>  
A;Cross-references: UNIPROT:P09636; GB:M18903; NID:g213797; PIDN:AAA49559.1; PID:g213798  
C;Superfamily: homeobox homology  
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation

F;2-58/Domain: homeobox homology <HOX>

Query Match 90.3%; Score 84; DB 2; Length 75;  
Best Local Similarity 93.8%; Pred. No. 6.8e-06;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RQIKWIFQNRMRMKWFK 16  
|||||  
Db 43 RQIKWIFQNRMRMKWKK 58

## RESULT 13

C43559  
homeotic protein R3 - rat (fragment)  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 16-Aug-2004  
C:Accession: C43559  
R:Falzon, M.; Chung, S.Y.  
Development 103, 601-610, 1988  
A:Title: The expression of rat homeobox-containing genes is developmentally regulated and  
A:Reference number: A43559; MUID:89231502; PMID:2907739  
A:Accession: C43559  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-76 <FAL>  
A:Cross-references: UNIPROT:P18865; GB:M37567; NID:g204634; PIDN:AAA41343.1; PID:g204635  
C:Superfamily: homeobox homology  
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation  
F;20-76/Domain: homeobox homology (fragment) <HOX>

Query Match 90.3%; Score 84; DB 2; Length 76;  
Best Local Similarity 93.8%; Pred. No. 6.9e-06;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RQIKWIFQNRMRMKWFK 16  
|||||  
Db 53 RQIKWIFQNRMRMKWKK 68

## RESULT 14

I51342  
homeo box protein - Atlantic salmon (fragment)  
C:Species: Salmo salar (Atlantic salmon)  
C:Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 16-Aug-2004  
C:Accession: I51342  
R:Fjose, A.; Molven, A.; Eiken, H.G.  
Gene 62, 141-152, 1988  
A:Title: Molecular cloning and characterization of homeobox-containing genes from Atlantic  
A:Reference number: I51341; MUID:88226009; PMID:2897318  
A:Accession: I51342  
A>Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-78 <FJO>  
A:Cross-references: UNIPROT:P09637; GB:M18904; NID:g213799; PIDN:AAA49560.1; PID:g213800  
C:Superfamily: homeobox homology  
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation  
F;2-58/Domain: homeobox homology <HOX>

Query Match 90.3%; Score 84; DB 2; Length 78;  
Best Local Similarity 93.8%; Pred. No. 7.1e-06;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RQIKWIFQNRMRMKWFK 16  
|||||  
Db 43 RQIKWIFQNRMRMKWKK 58

## RESULT 15

B29585  
homeotic protein Hox 2.2 precursor - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 15-Dec-1988 #sequence\_revision 30-Sep-1991 #text\_change 17-Oct-1997  
C:Accession: B29585

R:Lonai, P.; Arman, E.; Czosnek, H.; Ruddle, F.H.; Blatt, C.  
DNA 6, 409-418, 1987  
A:Title: New murine homeoboxes: structure, chromosomal assignment, and differential expr.  
A:Reference number: A29585; MUID:88054465; PMID:2890503  
A:Accession: B29585  
A:Molecule type: DNA  
A:Residues: 1-81 <LON>  
A:Cross-references: GB:M18167  
A:Note: the authors translated the codon CAG for residue 69 as Glu  
C:Superfamily: unassigned homeobox proteins; homeobox homology  
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation  
F;4-60/Domain: homeobox homology <HOX>

Query Match 90.3%; Score 84; DB 2; Length 81;  
Best Local Similarity 93.8%; Pred. No. 7.3e-06;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RQIKWIFQNRMRMKWFK 16  
|||||  
Db 45 RQIKWIFQNRMRMKWKK 60

Search completed: March 31, 2005, 00:31:37  
Job time : 3.09231 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 31, 2005, 00:19:36 ; Search time 8.92308 Seconds  
(without alignments)  
918.211 Million cell updates/sec

Title: US-10-049-822A-13  
Perfect score: 93  
Sequence: 1 RQIKWQNRRMKWFK 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	84	90.3	33	2 Q86FU0	Q86fu0 drosophila
2	84	90.3	39	2 O57368	O57368 brachydanio
3	84	90.3	42	2 Q80WH6	Q80wh6 rattus sp.
4	84	90.3	43	2 O57359	O57359 brachydanio
5	84	90.3	44	2 Q618J3	Q618j3 lampetra ja
6	84	90.3	46	2 Q9PVR9	Q9pvr9 oryzias lat
7	84	90.3	47	2 Q61T83	Q61t83 oncopeltus
8	84	90.3	48	1 HXB6 XENLA	P31256 xenopus lae
9	84	90.3	49	1 HXA5 SHEEP	Q28599 ovis aries
10	84	90.3	50	2 Q14543	Q14543 homo sapien
11	84	90.3	51	2 Q23743	Q23743 ctenodrilus
12	84	90.3	51	2 Q26407	Q26407 ctenodrilus
13	84	90.3	51	2 Q27413	Q27413 ctenodrilus
14	84	90.3	51	2 Q7JPR7	Q7jpr7 ctenodrilus
15	84	90.3	57	2 Q9PVR8	Q9pvr8 oryzias lat
16	84	90.3	58	2 Q25208	Q25208 junonia coe
17	84	90.3	58	2 Q9Y188	Q9y188 priapulid c
18	84	90.3	58	2 Q57362	O57362 brachydanio
19	84	90.3	59	2 Q8WRM9	Q8wr9 lithobius a
20	84	90.3	59	2 Q9NB42	Q9nb42 anopheles g
21	84	90.3	59	2 Q9PVR5	Q9pvr5 oryzias lat
22	84	90.3	60	2 Q77139	Q77139 archegozete
23	84	90.3	60	2 Q77143	Q77143 archegozete
24	84	90.3	60	2 Q80WH4	Q80wh4 rattus sp.
25	84	90.3	60	2 Q80WH7	Q80wh7 rattus sp.
26	84	90.3	60	2 Q8QGL2	Q8qgl2 petromyzon
27	84	90.3	60	2 Q8QGL3	Q8qgl3 petromyzon
28	84	90.3	60	2 Q8QGL5	Q8qgl5 petromyzon
29	84	90.3	60	2 Q8QGL6	Q8qgl6 petromyzon
30	84	90.3	60	2 Q8QGL7	Q8qgl7 petromyzon
31	84	90.3	60	2 Q8QGL8	Q8qgl8 petromyzon

32 84 90.3 61 2 Q27910 Q27910 polyandroca  
33 84 90.3 63 2 Q77138 Q77138 archegozete  
34 84 90.3 63 2 Q8MXB2 Q8mxb2 holopneuste  
35 84 90.3 66 2 O57356 O57356 brachydanio  
36 84 90.3 69 2 Q9BMF7 Q9bmf7 haliotis as  
37 84 90.3 69 2 Q9U9T4 Q9ugt4 nereis vire  
38 84 90.3 70 2 Q967W5 Q967w5 folsomia ca  
39 84 90.3 70 2 Q801B4 Q801b4 latimeria m  
40 84 90.3 71 1 HXA7 SHEEP Q28600 ovis aries  
41 84 90.3 71 1 HXC5 NOTVI P31262 notophthalm  
42 84 90.3 71 2 Q6EBC8 Q6ebc8 bugula turr  
43 84 90.3 71 2 Q9PVS1 Q9pvs1 oryzias lat  
44 84 90.3 71 2 Q9PVS3 Q9pvs3 oryzias lat  
45 84 90.3 73 2 Q86D93 Q86d93 spadella ce

#### ALIGNMENTS

RESULT 1  
Q86FU0  
ID Q86FU0 PRELIMINARY; PRT; 33 AA.  
AC O86FU0;  
DT 01-JUN-2003 (TREMBLrel. 24, Created)  
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)  
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
DE Antennapedia complex (Fragment).  
GN Name=ANT-C;  
OS Drosophila pseudoobscura (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7237;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=9322933; PubMed=8099892;  
RA Randazzo F.M., Seeger M.A., Huss C.A., Sweeney M.A., Cecil J.K.,  
RA Kaufman T.C.;  
RT "Structural changes in the antennapedia complex of Drosophila  
pseudoobscura.";  
RL Genetics 134:319-330(1993).  
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).  
DR EMBL; S63455; AAP13946.1; -.  
DR HSSP; P02833; 1HOM.  
DR GO; GO:0005634; C:nucleus; IEA.  
DR GO; GO:0003700; F:transcription factor activity; IEA.  
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
DR InterPro; IPR001356; Homeobox.  
DR InterPro; IPR009057; Homeodomain\_like.  
DR PRINTS; PR00024; HOMEBOX.  
DR ProDom; PD000010; Homeobox; 1.  
DR PROSITE; PS00071; HOMEBOX 2; 1.  
KW DNA-binding; Homeobox; Nuclear protein.  
FT NON\_TER 1  
FT NON\_TER 33  
SQ SEQUENCE 33 AA; 3963 MW; D78E37ED81FD45DF CRC64;

Query Match 90.3%; Score 84; DB 2; Length 33;  
Best Local Similarity 93.8%; Pred. No. 8.4e-06;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RQIKWQNRRMKWFK 16  
|||||  
Db 7 RQIKWQNRRMKWKK 22

#### RESULT\*2

O57368  
ID O57368 PRELIMINARY; PRT; 39 AA.  
AC O57368;  
DT 01-JUN-1998 (TREMBLrel. 06, Created)  
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)  
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

DE Hoxc5 protein (Fragment).  
GN Name=hoxc5a; Synonyms=hoxc5;  
OS Brachydanio rerio (Zebrafish) (Danio rerio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Prince V.E., Joly L., Ekker M., Ho R.K.;  
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.  
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).  
DR EMBL; Y14539; CAA74874.1; -.  
DR HSSP; P02833; 1HOM.  
DR ZFIN; ZDB-GENE-980526-533; hoxc5a.  
DR GO; GO:0005634; C:nucleus; IEA.  
DR GO; GO:0003700; F:transcription factor activity; IEA.  
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
DR InterPro; IPR001356; Homeobox.  
DR InterPro; IPR009057; Homeodomain-like.  
DR InterPro; IPR000047; HTH\_lambrepresr.  
DR Pfam; PF000046; Homeobox; 1.  
DR PRINTS; PR00024; HOMEBOX.  
DR PRODOM; PD000010; Homeobox; 1.  
DR SMART; SM00389; HOX; 1.  
DR PROSITE; PS00027; HOMEBOX\_1; 1.  
DR PROSITE; PS00071; HOMEBOX\_2; 1.  
KW DNA-binding; Homeobox; Nuclear protein.  
FT NON\_TER 1  
SQ SEQUENCE 39 AA; 4827 MW; 592A0FEC12B58860 CRC64;

Query Match 90.3%; Score 84; DB 2; Length 39;  
Best Local Similarity 93.8%; Pred. No. 1e-05;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RQIKWIFQNRMRMKWFK 16  
| | | | | | | | | | | | | | | | | |  
Db 14 RQIKWIFQNRMRMKW 29

RESULT 3  
Q80WH6 PRELIMINARY; PRT; 42 AA.  
AC Q80WH6;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Hox-A|Hox-1 (Fragment).  
GN Name=Hox-A|Hox-1;  
OS Rattus sp.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10118;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA MEDLINE=95217128; PubMed=7702549;  
RA Sakoyama Y., Mizuta I., Ogasawara N., Yoshikawa H.;  
RT "Cloning of rat homeobox genes."  
RL Biochem. Genet. 32:351-360(1994).  
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).  
DR EMBL; S76290; AAP31864.1; -.  
DR HSSP; P02833; 1HOM.  
DR GO; GO:0005634; C:nucleus; IEA.  
DR GO; GO:0003700; F:transcription factor activity; IEA.  
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
DR InterPro; IPR001356; Homeobox.  
DR InterPro; IPR009057; Homeodomain-like.  
DR InterPro; IPR000047; HTH\_lambrepresr.  
DR Pfam; PF000046; Homeobox; 1.  
DR PRINTS; PR00024; HOMEBOX.  
DR PRODOM; PD000010; Homeobox; 1.

DR SMART; SM00389; HOX; 1.  
DR PROSITE; PS00027; HOMEBOX\_1; 1.  
DR PROSITE; PS00071; HOMEBOX\_2; 1.  
KW DNA-binding; Homeobox; Nuclear protein.  
FT NON\_TER 1  
FT NON\_TER 42  
SQ SEQUENCE 42 AA; 5494 MW; 38B5153B92216FE9 CRC64;

Query Match 90.3%; Score 84; DB 2; Length 42;  
Best Local Similarity 93.8%; Pred. No. 1.1e-05;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RQIKWIFQNRMRMKWFK 16  
| | | | | | | | | | | | | | | | | |  
Db 25 RQIKWIFQNRMRMKWK 40

RESULT 4  
O57359 PRELIMINARY; PRT; 43 AA.  
AC O57359;  
DT 01-JUN-1998 (TrEMBLrel. 06, Created)  
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Hoxa5 protein (Fragment).  
GN Name=hoxb5b; Synonyms=hoxa5;  
OS Brachydanio rerio (Zebrafish) (Danio rerio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Prince V.E., Joly L., Ekker M., Ho R.K.;  
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.  
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).  
DR EMBL; Y14526; CAA74861.1; -.  
DR HSSP; P02833; 1HOM.  
DR ZFIN; ZDB-GENE-000823-6; hoxb5b.  
DR GO; GO:0005634; C:nucleus; IEA.  
DR GO; GO:0003700; F:transcription factor activity; IEA.  
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
DR InterPro; IPR001356; Homeobox.  
DR InterPro; IPR009057; Homeodomain-like.  
DR Pfam; PF000046; Homeobox; 1.  
DR PRINTS; PR00024; HOMEBOX.  
DR PRODOM; PD000010; Homeobox; 1.  
DR PROSITE; PS00027; HOMEBOX\_1; 1.  
DR PROSITE; PS00071; HOMEBOX\_2; 1.  
KW DNA-binding; Homeobox; Nuclear protein.  
FT NON\_TER 1  
SQ SEQUENCE 43 AA; 5050 MW; 53034C37F3DFA596 CRC64;

Query Match 90.3%; Score 84; DB 2; Length 43;  
Best Local Similarity 93.8%; Pred. No. 1.1e-05;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RQIKWIFQNRMRMKWFK 16  
| | | | | | | | | | | | | | | | | |  
Db 10 RQIKWIFQNRMRMKWK 25

RESULT 5  
Q6L8J3 PRELIMINARY; PRT; 44 AA.  
AC Q6L8J3;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE LjHox7m Homeobox (Fragment).  
GN Name=LjHox7m;  
OS Lampetra japonica (Japanese lamprey) (Entosphenus japonicus).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;



OC Petromyzontiformes; Petromyzontidae; Lethenteron.  
 RN NCBI\_TaxID=94989;  
 RP SEQUENCE FROM N.A.  
 RA Takio Y., Kuraku S., Kuratani S.;  
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.  
 CC -I- SUBCELLULAR LOCATION: Nuclear (By similarity).  
 DR EMBL; AB125272; BAD2526.1; -.  
 DR HSSP; P02833; LAHD.  
 DR GO; GO:0005634; C:nucleus; IEA.  
 DR GO; GO:0003700; F:transcription factor activity; IEA.  
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro; IPR001356; Homeobox.  
 DR InterPro; IPR009057; Homeobox-like.  
 DR InterPro; IPR000047; HTH lambrpressor.  
 DR Pfam; PF00046; Homeobox\_1.  
 DR PRINTS; PR00024; HOMEBOX.  
 DR PRODOM; PD000010; Homeobox; 1.  
 DR SMART; SM00389; HOX; 1.  
 DR PROSITE; PS00027; HOMEBOX 1; 1.  
 DR PROSITE; PS00071; HOMEBOX\_2; 1.  
 KW DNA-binding; Homeobox; Nuclear protein.  
 FT NON TER 1 1  
 FT NON TER 44 44  
 SQ SEQUENCE 44 AA; 5668 MW; B608B0F91C51ED11 CRC64;

Query Match 90.3%; Score 84; DB 2; Length 44;  
 Best Local Similarity 93.8%; Pred. No. 1.1e-05;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RQIKWIFQNRMRKWK 16  
 Db 23 RQIKWIFQNRMRKWK 38  
 |||||

RESULT 6  
 Q9PVR9 PRELIMINARY; PRT; 46 AA.  
 AC Q9PVR9;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
 DE HOXC5A (Fragment).  
 GN Name=hoxc5a;  
 OS Oryzias latipes (Medaka fish) (Japanese ricefish).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;  
 OC Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.  
 OX NCBI\_TaxID=8090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Kondo S., Naruse K., Shima A.;  
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
 CC -I- SUBCELLULAR LOCATION: Nuclear (By similarity).  
 DR EMBL; AB026960; BAA86243.1; -.  
 DR HSSP; P02833; 9ANT.  
 DR GO; GO:0005634; C:nucleus; IEA.  
 DR GO; GO:0003700; F:transcription factor activity; IEA.  
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro; IPR001356; Homeobox.  
 DR InterPro; IPR009057; Homeobox-like.  
 DR Pfam; PF00046; Homeobox; 1.  
 DR PRINTS; PR00024; HOMEBOX.  
 DR PRODOM; PD000010; Homeobox; 1.  
 DR SMART; SM00389; HOX; 1.  
 DR PROSITE; PS00027; HOMEBOX 1; 1.  
 DR PROSITE; PS00071; HOMEBOX\_2; 1.  
 KW DNA-binding; Homeobox; Nuclear protein.  
 FT NON TER 1 1  
 FT NON TER 46 46  
 SQ SEQUENCE 46 AA; 5955 MW; 6039999ED4294DD3 CRC64;

Query Match 90.3%; Score 84; DB 2; Length 46;  
 Best Local Similarity 93.8%; Pred. No. 1.2e-05;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RQIKWIFQNRMRKWK 16  
 Db 23 RQIKWIFQNRMRKWK 38  
 |||||

RESULT 7  
 Q6IT83 PRELIMINARY; PRT; 47 AA.  
 AC Q6IT83;  
 DT 05-JUL-2004 (TREMBlrel. 27, Created)  
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
 DE Antennapedia (Fragment).  
 OS Oncopeltus fasciatus (Milkweed bug).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Paraneoptera; Hemiptera; Euhemiptera; Heteroptera;  
 OC Panheteroptera; Pentatomomorpha; Lygaeoidea; Lygaeinae;  
 OC Oncopeltus.  
 OX NCBI\_TaxID=7536;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Liu P.Z., Kaufman T.C.;  
 RL "Kruppel is a gap gene in the intermediate germband insect *Oncopeltus* fasciatus and is required for development of both blastoderm and germband-derived segments.";  
 RL Development 131:4567-4579(2004).  
 CC -I- SUBCELLULAR LOCATION: Nuclear (By similarity).  
 DR EMBL; AY627363; AAT44525.1; -.  
 DR HSSP; P02833; LAHD.  
 DR GO; GO:0005634; C:nucleus; IEA.  
 DR GO; GO:0003700; F:transcription factor activity; IEA.  
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro; IPR001356; Homeobox.  
 DR InterPro; IPR009057; Homeobox-like.  
 DR Pfam; PF00046; Homeobox; 1.  
 DR PRINTS; PR00024; HOMEBOX.  
 DR PRODOM; PD000010; Homeobox; 1.  
 DR PROSITE; PS00071; HOMEBOX\_2; 1.  
 KW DNA-binding; Homeobox; Nuclear protein.  
 FT NON TER 1 1  
 SQ SEQUENCE 47 AA; 5441 MW; ABBAE19564222859 CRC64;

Query Match 90.3%; Score 84; DB 2; Length 47;  
 Best Local Similarity 93.8%; Pred. No. 1.2e-05;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RQIKWIFQNRMRKWK 16  
 Db 9 RQIKWIFQNRMRKWK 24  
 |||||

RESULT 8  
 HXB6 XENLA STANDARD; PRT; 48 AA.  
 AC P31256;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Homeobox protein Hox-B6 (XlHox-2.2) (Fragment).  
 GN Name=HXB6; Synonyms=XLHox-2.2;  
 OS *Xenopus laevis* (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OX NCBI\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=93043517; PubMed=1384809;

RA Leroy P., de Robertis E.M.;  
RT "Effects of lithium chloride and retinoic acid on the expression of  
RL genes from the *Xenopus laevis* Hox 2 complex.";   
RL Dev. Dyn. 194;21:32(1992).  
CC -!- FUNCTION: Sequence-specific transcription factor which is part of  
CC a developmental regulatory system that provides cells with  
CC specific positional identities on the anterior-posterior axis.  
CC -!- SUBCELLULAR LOCATION: Nuclear.  
CC -!- SIMILARITY: Belongs to the Antp homeobox family.  
CC -!- SIMILARITY: Contains 1 homeobox domain.  
CC -----  
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CC -----  
CC EMBL; M91587; AAA49750.1; -.  
DR PIR; I51439; I51439.  
DR HSSP; P02833; IHOM.  
DR InterPro; IPR001827; Antennapedia.  
DR InterPro; IPR001356; Homeobox.  
DR InterPro; IPR009057; Homeobox\_like.  
DR Pfam; PF00046; Homeobox; 1.  
DR PRINTS; PR00024; HOMEBOX.  
DR PRODOM; PD000010; Homeobox; 1.  
DR SMART; SM00389; HOX; 1.  
DR PROSITE; PS00027; HOMEBOX 1; 1.  
DR PROSITE; PS50071; HOMEBOX 2; 1.  
DR PROSITE; PS50071; HOMEBOX 2; 1.  
KW Developmental protein; DNA-binding; Homeobox; Nuclear protein;  
KW Transcription regulation.  
FT NON TER 1 1  
FT DNA\_BIND <1 29 Homeobox.  
FT NON TER 1 1  
SQ SEQUENCE 48 AA; 5716 MW; BC39E36822EDDD2A CRC64;  
  
Query Match 90.3%; Score 84; DB 1; Length 48;  
Best Local Similarity 93.8%; Pred. No. 1.2e-05;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 1 RQIKWFFQNRRMKWFK 16  
Db 12 RQIKWFFQNRRMKWKK 27  
  
RESULT 9  
HXAS SHEEP STANDARD; PRT; 49 AA.  
AC Q28559;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Homeobox protein Hox-A5 (Fragment).  
CN Name=HOXA5; Synonyms=HOXA-5;  
OS Ovis aries (Sheep).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Caprinae; Ovis.  
OX NCBI\_TaxID=9940;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Roche P.J.;  
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: Sequence-specific transcription factor which is part of  
CC a developmental regulatory system that provides cells with  
CC specific positional identities on the anterior-posterior axis.  
CC Also binds to its own promoter. Binds specifically to the motif  
CC 5'-CYNATTA[TG]Y-3'.  
CC -!- SUBCELLULAR LOCATION: Nuclear.  
CC -!- SIMILARITY: Belongs to the Antp homeobox family.  
CC -!- SIMILARITY: Contains 1 homeobox domain.

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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL; U61978; AAB04754.1; -.  
DR HSSP; P02833; IHOM.  
DR InterPro; IPR001356; Homeobox.  
DR InterPro; IPR009057; Homeobox\_like.  
DR Pfam; PF00046; Homeobox; 1.  
DR PRINTS; PR00024; HOMEBOX.  
DR PRODOM; PD000010; Homeobox; 1.  
DR SMART; SM00389; HOX; 1.  
DR PROSITE; PS00027; HOMEBOX 1; 1.  
DR PROSITE; PS50071; HOMEBOX 2; 1.  
DR PROSITE; PS50071; HOMEBOX 2; 1.  
KW Developmental protein; DNA-binding; Homeobox; Nuclear protein;  
KW Transcription regulation.  
FT NON TER 1 1  
FT DNA\_BIND <1 49 Homeobox.  
FT NON TER 49 49  
SQ SEQUENCE 49 AA; 6331 MW; 1EE702315E7C099B CRC64;  
  
Query Match 90.3%; Score 84; DB 1; Length 49;  
Best Local Similarity 93.8%; Pred. No. 1.3e-05;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 1 RQIKWFFQNRRMKWFK 16  
Db 32 RQIKWFFQNRRMKWKK 47  
  
RESULT 10  
Q14543 PRELIMINARY; PRT; 50 AA.  
ID Q14543  
AC Q14543;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Homeobox protein (50 AA) (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RA Gilman J.G.;  
RL Submitted (APR-1990) to the EMBL/GenBank/DBJ databases.  
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).  
DR EMBL; X52402; CAA36647.1; -.  
DR PIR; S10907; S10907.  
DR HSSP; P02833; 9ANT.  
DR GO; GO:0005634; C:nucleus; IEA.  
DR GO; GO:0003700; F:transcription factor activity; IEA.  
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
DR InterPro; IPR001356; Homeobox.  
DR InterPro; IPR009057; Homeobox\_like.  
DR Pfam; PF00046; Homeobox; 1.  
DR PRINTS; PR00024; HOMEBOX.  
DR PRODOM; PD000010; Homeobox; 1.  
DR SMART; SM00389; HOX; 1.  
DR PROSITE; PS00027; HOMEBOX 1; 1.  
DR PROSITE; PS50071; HOMEBOX 2; 1.  
KW DNA-binding; Homeobox; Nuclear protein.  
FT NON TER 1 1  
SQ SEQUENCE 50 AA; 6411 MW; 9E90625E455ED582 CRC64;  
  
Query Match 90.3%; Score 84; DB 2; Length 50;  
Best Local Similarity 93.8%; Pred. No. 1.3e-05;

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Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ROIKIWFQNRMRKWK 16
Db 25 ROIKIWFQNRMRKWK 40

RESULT 11
Q23743 ID Q23743 PRELIMINARY; PRT; 51 AA.
AC Q23743;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Deformed ortholog homeobox (Fragment).
GN Name=CTS-Dfd;
OS Ctenodrilus serratus.
OC Eukaryota; Metazoa; Annelida; Polychaeta; Palpata; Canaliculipalata;
OC Terebellida; Ctenodrilidae; Ctenodrilus.
OX NCBI_TaxID=40316;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94356262; PubMed=7915607; DOI=10.1006/mpev.1994.1017;
RA "A PCR-based survey of homeobox genes in Ctenodrilus serratus
RT (Annelida: Polychaeta).";
RL Mol. Phylogenet. Evol. 3:146-158(1994).
CC -I- SUBCELLULAR LOCATION: Nuclear (By similarity).
DR HSSP; P02833; 9ANT.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR009057; HTH lambdarepressor.
DR Pfam; PF00046; Homeobox_1.
DR PRINTS; PR00024; HOMEBOX.
DR PRINTS; PR00031; HTHREPRESSR.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS00071; HOMEBOX_2; 1.
KW DNA-binding; Homeobox; Nuclear protein.
FT NON_TER 1 51
FT NON_TER 1 51
SQ SEQUENCE 51 AA; 6533 MW; 9EDB50C927FECBD5 CRC64;

Query Match 90.3%; Score 84; DB 2; Length 51;
Best Local Similarity 93.8%; Pred. No. 1.3e-05;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ROIKIWFQNRMRKWK 16
Db 23 ROIKIWFQNRMRKWK 38

RESULT 13
Q27413 ID Q27413 PRELIMINARY; PRT; 51 AA.
AC Q27413;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Lox5 ortholog homeobox (Fragment).
GN Name=CTS-Lox5;
OS Ctenodrilus serratus.
OC Eukaryota; Metazoa; Annelida; Polychaeta; Palpata; Canaliculipalata;
OC Terebellida; Ctenodrilidae; Ctenodrilus.
OX NCBI_TaxID=40316;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94356262; PubMed=7915607; DOI=10.1006/mpev.1994.1017;
RA "A PCR-based survey of homeobox genes in Ctenodrilus serratus
RT (Annelida: Polychaeta).";
RL Mol. Phylogenet. Evol. 3:146-158(1994).
RN [2]
RP SEQUENCE FROM N.A.
RA Dick M.H., Buss L.W.;
RA Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
CC -I- SUBCELLULAR LOCATION: Nuclear (By similarity).
DR HSSP; P02833; 9ANT.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR009057; HTH lambdarepressor.
DR Pfam; PF00046; Homeobox_1.
DR PRINTS; PR00024; HOMEBOX.
DR PRINTS; PR00031; HTHREPRESSR.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS00071; HOMEBOX_2; 1.
KW DNA-binding; Homeobox; Nuclear protein.
FT NON_TER 1 51
FT NON_TER 1 51
SQ SEQUENCE 51 AA; 6533 MW; 9EDB50C927FECBD5 CRC64;

Query Match 90.3%; Score 84; DB 2; Length 51;
Best Local Similarity 93.8%; Pred. No. 1.3e-05;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ROIKIWFQNRMRKWK 16
Db 23 ROIKIWFQNRMRKWK 38

RESULT 12
Q26407 ID Q26407 PRELIMINARY; PRT; 51 AA.
AC Q26407;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE CTS-Dfd protein (Fragment).
GN Name=CTS-Dfd;
OS Ctenodrilus serratus.
OC Eukaryota; Metazoa; Annelida; Polychaeta; Palpata; Canaliculipalata;
OC Terebellida; Ctenodrilidae; Ctenodrilus.
OX NCBI_TaxID=40316;
```

```
[1]
SEQUENCE FROM N.A.
MEDLINE=94356262; PubMed=7915607; DOI=10.1006/mpev.1994.1017;
Dick M.H., Buss L.W.;
"A PCR-based survey of homeobox genes in Ctenodrilus serratus
(Annelida: Polychaeta).";
Mol. Phylogenet. Evol. 3:146-158(1994).
-I- SUBCELLULAR LOCATION: Nuclear (By similarity).
EMBL; S76416; AAB31775.1; -.
HSSP; P02833; 9ANT.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR001356; Homeobox.
InterPro; IPR009057; HTH lambdarepressor.
Pfam; PF00046; Homeobox; 1.
PRINTS; PR00024; HOMEBOX.
PRINTS; PR00031; HTHREPRESSR.
PROSITE; PS00027; HOMEBOX_1; 1.
PROSITE; PS00071; HOMEBOX_2; 1.
KW DNA-binding; Homeobox; Nuclear protein.
FT NON_TER 51 51
SQ SEQUENCE 51 AA; 6533 MW; 9EDB50C927FECBD5 CRC64;

Query Match 90.3%; Score 84; DB 2; Length 51;
Best Local Similarity 93.8%; Pred. No. 1.3e-05;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ROIKIWFQNRMRKWK 16
Db 23 ROIKIWFQNRMRKWK 38

RESULT 13
Q27413 ID Q27413 PRELIMINARY; PRT; 51 AA.
AC Q27413;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Lox5 ortholog homeobox (Fragment).
GN Name=CTS-Lox5;
OS Ctenodrilus serratus.
OC Eukaryota; Metazoa; Annelida; Polychaeta; Palpata; Canaliculipalata;
OC Terebellida; Ctenodrilidae; Ctenodrilus.
OX NCBI_TaxID=40316;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94356262; PubMed=7915607; DOI=10.1006/mpev.1994.1017;
RA "A PCR-based survey of homeobox genes in Ctenodrilus serratus
RT (Annelida: Polychaeta).";
RL Mol. Phylogenet. Evol. 3:146-158(1994).
RN [2]
RP SEQUENCE FROM N.A.
RA Dick M.H., Buss L.W.;
RA Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
CC -I- SUBCELLULAR LOCATION: Nuclear (By similarity).
DR HSSP; P02833; 9ANT.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR001356; Homeobox.
InterPro; IPR009057; HTH lambdarepressor.
Pfam; PF00046; Homeobox; 1.
PRINTS; PR00024; HOMEBOX.
PRINTS; PR00031; HTHREPRESSR.
PRODOM; PD000010; Homeobox; 1.
SMART; SM00389; HOX; 1.
PROSITE; PS00027; HOMEBOX_1; 1.
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DR PROSITE, PS0071; HOMEBOX 2; 1.
KW DNA-binding; Homeobox; Nuclear protein.
FT NON_TER 1 1
FT NON_TER 51 51
SQ SEQUENCE 51 AA; 6278 MW; 88C8F65161E94A22 CRC64;

Query Match          90.3%; Score 84; DB 2; Length 51;
Best Local Similarity 93.8%; Pred. No. 1.3e-05;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RQIKIWQNRRMKWFK 16
Db 23 RQIKIWQNRRMKWKK 38

RESULT 14
QJUPR7 PRELIMINARY; PRT; 51 AA.
AC Q7JUPR7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE CTS-Lox5 protein (Fragment).
GN Name=CTS-Lox5;
OS Ctenodrilus serratus.
OC Eukaryota; Metazoa; Annelida; Polychaeta; Palpata; Canalipalpata;
OC Terebellida; Ctenodrilidae; Ctenodrilus.
OX NCBI_TaxID=40316;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94356262; PubMed=7915607; DOI=10.1006/mpev.1994.1017;
RA Dick M.H., Buss L.W.;
RT "A PCR-based survey of homeobox genes in Ctenodrilus serratus
  (Annelida: Polychaeta).";
RL Mol. Phylogenet. Evol. 3:146-158(1994).
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
DR EMBL; S76226; AAB31777.1; -.
DR HSSP; P83949; 1B8I.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR009057; Homeodomain like.
DR InterPro; IPR000047; HTH_lambrepresr.
DR Pfam; PF00046; Homeobox_1.
DR PRINTS; PR00024; HOMEBOX.
DR PRODOM; PD00010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX 1; 1.
DR PROSITE; PS50071; HOMEBOX_2; 1.
KW DNA-binding; Homeobox; Nuclear protein.
FT NON_TER 51 51
SQ SEQUENCE 51 AA; 6278 MW; 88C8F65161E94A22 CRC64;

Query Match          90.3%; Score 84; DB 2; Length 51;
Best Local Similarity 93.8%; Pred. No. 1.3e-05;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RQIKIWQNRRMKWFK 16
Db 23 RQIKIWQNRRMKWKK 38

RESULT 15
Q9PVR8 PRELIMINARY; PRT; 57 AA.
AC Q9PVR8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE HOXA5A (Fragment).
GN Name=hoxa5a;

OS Oryzias latipes (Medaka fish) (Japanese ricefish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.
OX NCBI_TaxID=8090;
[1]
RP SEQUENCE FROM N.A.
RA Kondo S., Naruse K., Shima A.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
DR EMBL; AB026961; BAA86244.1; -.
DR HSSP; P02833; 1HOM.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR009057; Homeodomain like.
DR Pfam; PF00046; Homeobox; 1.
DR PRINTS; PR00024; HOMEBOX.
DR PRODOM; PD00010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX 1; 1.
DR PROSITE; PS50071; HOMEBOX_2; 1.
KW DNA-binding; Homeobox; Nuclear protein.
FT NON_TER 1 1
SQ SEQUENCE 57 AA; 6891 MW; 54A6430320F68C04 CRC64;

Query Match          90.3%; Score 84; DB 2; Length 57;
Best Local Similarity 93.8%; Pred. No. 1.5e-05;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RQIKIWQNRRMKWFK 16
Db 23 RQIKIWQNRRMKWKK 38

Search completed: March 31, 2005, 00:30:55
Job time : 11.9231 secs
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OM protein - protein search, using sw model

Run on: March 31, 2005, 00:25:06 ; Search time 5.28846 Seconds  
(without alignments)  
688.690 Million cell updates/sec

Title: US-10-049-822A-12  
Perfect score: 58  
Sequence: 1 YGRKKRQRRR 11

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1407402 seqs, 331100923 residues

Total number of hits satisfying chosen parameters: 1407402

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*  
1: /cgn2\_6/ptodata/2/pubaa/PCT\_NEW\_PUB.pdb.\*  
2: /cgn2\_6/ptodata/2/pubaa/PCT\_NEW\_PUB.pdb.\*  
3: /cgn2\_6/ptodata/2/pubaa/US06\_NEW\_PUB.pdb.\*  
4: /cgn2\_6/ptodata/2/pubaa/US06\_PUBCOMB.pdb.\*  
5: /cgn2\_6/ptodata/2/pubaa/US07\_NEW\_PUB.pdb.\*  
6: /cgn2\_6/ptodata/2/pubaa/PCTUS\_PUBCOMB.pdb.\*  
7: /cgn2\_6/ptodata/2/pubaa/US08\_NEW\_PUB.pdb.\*  
8: /cgn2\_6/ptodata/2/pubaa/US08\_PUBCOMB.pdb.\*  
9: /cgn2\_6/ptodata/2/pubaa/US09A\_PUBCOMB.pdb.\*  
10: /cgn2\_6/ptodata/2/pubaa/US09B\_PUBCOMB.pdb.\*  
11: /cgn2\_6/ptodata/2/pubaa/US09C\_PUBCOMB.pdb.\*  
12: /cgn2\_6/ptodata/2/pubaa/US09\_NEW\_PUB.pdb.\*  
13: /cgn2\_6/ptodata/2/pubaa/US10A\_PUBCOMB.pdb.\*  
14: /cgn2\_6/ptodata/2/pubaa/US10B\_PUBCOMB.pdb.\*  
15: /cgn2\_6/ptodata/2/pubaa/US10C\_PUBCOMB.pdb.\*  
16: /cgn2\_6/ptodata/2/pubaa/US10D\_PUBCOMB.pdb.\*  
17: /cgn2\_6/ptodata/2/pubaa/US10\_NEW\_PUB.pdb.\*  
18: /cgn2\_6/ptodata/2/pubaa/US11\_NEW\_PUB.pdb.\*  
19: /cgn2\_6/ptodata/2/pubaa/US60\_NEW\_PUB.pdb.\*  
20: /cgn2\_6/ptodata/2/pubaa/US60\_PUBCOMB.pdb.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	58	100.0	11	9	US-09-779-791A-1
2	58	100.0	11	9	US-09-780-070-37
3	58	100.0	11	9	US-09-815-108-9
4	58	100.0	11	9	US-09-886-404-13
5	58	100.0	11	9	US-09-805-805-8
6	58	100.0	11	9	US-09-821-821-24
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14	58	100.0	11	9	US-09-984-183-4	Sequence 4, Appli
15	58	100.0	11	9	US-09-949-196-15	Sequence 15, Appl
16	58	100.0	11	9	US-09-948-018-22	Sequence 22, Appl
17	58	100.0	11	9	US-09-995-515-14	Sequence 14, Appl
18	58	100.0	11	9	US-09-895-593-13	Sequence 13, Appl
19	58	100.0	11	9	US-09-896-738-20	Sequence 20, Appl
20	58	100.0	11	9	US-09-981-286A-2	Sequence 2, Appli
21	58	100.0	11	10	US-09-134-793-2	Sequence 2, Appli
22	58	100.0	11	10	US-09-882-291-43	Sequence 43, Appl
23	58	100.0	11	10	US-09-775-052-2	Sequence 2, Appli
24	58	100.0	11	10	US-09-847-946A-124	Sequence 124, App
25	58	100.0	11	10	US-09-847-946A-125	Sequence 125, App
26	58	100.0	11	10	US-09-876-904A-5	Sequence 5, Appli
27	58	100.0	11	10	US-09-876-904A-10	Sequence 10, Appl
28	58	100.0	11	10	US-09-845-612B-20	Sequence 20, Appl
29	58	100.0	11	10	US-09-997-465B-2	Sequence 2, Appli
30	58	100.0	11	10	US-09-911-261A-18	Sequence 18, Appl
31	58	100.0	11	10	US-09-798-053-10	Sequence 10, Appl
32	58	100.0	11	12	US-09-779-791A-1	Sequence 1, Appli
33	58	100.0	11	13	US-10-007-363-5	Sequence 5, Appli
34	58	100.0	11	14	US-10-139-833-18	Sequence 18, Appl
35	58	100.0	11	14	US-10-142-356-23	Sequence 23, Appl
36	58	100.0	11	14	US-10-156-424A-14	Sequence 14, Appl
37	58	100.0	11	14	US-10-208-374-2	Sequence 2, Appli
38	58	100.0	11	14	US-10-156-932-42	Sequence 42, Appl
39	58	100.0	11	14	US-10-077-555-4	Sequence 4, Appli
40	58	100.0	11	14	US-10-057-408-18	Sequence 18, Appl
41	58	100.0	11	14	US-10-229-915-28	Sequence 28, Appl
42	58	100.0	11	14	US-10-229-584-9	Sequence 9, Appli
43	58	100.0	11	14	US-10-156-487A-7	Sequence 7, Appli
44	58	100.0	11	14	US-10-193-616-15	Sequence 15, Appl
45	58	100.0	11	14	US-10-251-947-9	Sequence 9, Appli

#### ALIGNMENTS

RESULT 1  
US-09-779-791A-1  
; Sequence 1, Application US/09779791A  
; Publication No. US2001004417A1  
; GENERAL INFORMATION:  
; APPLICANT: Mirus Corporation  
; APPLICANT: Wolff, Jon A  
; APPLICANT: Monahan, Sean D  
; APPLICANT: Budker, Vladimir G  
; APPLICANT: Slattum, Paul M  
; APPLICANT: Rozema, David B  
; TITLE OF INVENTION: A Compound Containing a Labile Disulfide Bond  
; FILE REFERENCE: Mirus.006.03  
; CURRENT APPLICATION NUMBER: US/09/779,791A  
; CURRENT FILING DATE: 2001-02-08  
; PRIOR APPLICATION NUMBER: 09/312,351  
; PRIOR FILING DATE: 1999-05-14  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus  
US-09-779-791A-1

Query Match 100.0%; Score 58; DB 9; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.018;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 YGRKKRQRRR 11

RESULT 2  
US-09-780-070-37

; Sequence 37, Application US/09780070  
; Patent No. US20020009752A1  
; GENERAL INFORMATION:  
; APPLICANT: Burke, James  
; APPLICANT: Strittmatter, Warren  
; APPLICANT: Nagai, Yoshitaka  
; TITLE OF INVENTION: COMPOUNDS THAT SELECTIVELY BIND TO EXPANDED POLYGLUTAMINE REPEAT  
; FILE REFERENCE: 5405.242  
; CURRENT APPLICATION NUMBER: US/09/780,070  
; CURRENT FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: 60/189,781  
; PRIOR FILING DATE: 2000-03-16  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 37  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus  
US-09-780-070-37

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Best Local Similarity 100.0%; Pred. No. 0.018;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 YGRKKRQRRR 11

## RESULT 3

US-09-815-108-9  
; Sequence 9, Application US/09815108  
; Patent No. US20020009776A1  
; GENERAL INFORMATION:  
; APPLICANT: Saris, Christiaan M.  
; APPLICANT: Sharon, Mu X.  
; APPLICANT: Xia, Min  
; APPLICANT: Boone, Thomas Charles  
; APPLICANT: Covey, Todd  
; TITLE OF INVENTION: Fibroblast Growth Factor Receptor-Like Molecules and  
; FILE REFERENCE: 99-513-A  
; CURRENT APPLICATION NUMBER: US/09/815,108  
; CURRENT FILING DATE: 2001-03-22  
; PRIOR APPLICATION NUMBER: 60/191,379  
; PRIOR FILING DATE: 2000-03-22  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus type 1  
US-09-815-108-9

Query Match 100.0%; Score 58; DB 9; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.018;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 YGRKKRQRRR 11

## RESULT 4

US-09-886-404-13  
; Sequence 13, Application US/09886404  
; Patent No. US2002003752A1  
; GENERAL INFORMATION:  
; APPLICANT: Medlock, Eugene  
; APPLICANT: Yeh, Richard  
; APPLICANT: Silbiger, Scott M.  
; APPLICANT: Elliot, Gary S.

; APPLICANT: Nguyen, Hung Q.  
; APPLICANT: Jing, Shugian  
; TITLE OF INVENTION: IL-17 Like Molecules and Uses Thereof  
; FILE REFERENCE: 01017/37128B  
; CURRENT APPLICATION NUMBER: US/09/886,404  
; CURRENT FILING DATE: 2001-06-21  
; PRIOR APPLICATION NUMBER: 09/810,384  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/266,159  
; PRIOR FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: 60/213,125  
; PRIOR FILING DATE: 2000-06-22  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: PatentIn Ver. 2.0  
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; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide of HIV  
; OTHER INFORMATION: TAT protein  
US-09-886-404-13

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Best Local Similarity 100.0%; Pred. No. 0.018;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 YGRKKRQRRR 11

## RESULT 5

US-09-805-805-8  
; Sequence 8, Application US/09805805  
; Patent No. US20020037557A1  
; GENERAL INFORMATION:  
; APPLICANT: Bass, Michael B.  
; APPLICANT: Jing, Shugian  
; TITLE OF INVENTION: Fibroblast Growth Factor-Like Molecules and Uses  
; FILE REFERENCE: 01-006-A1  
; CURRENT APPLICATION NUMBER: US/09/805,805  
; CURRENT FILING DATE: 2001-03-13  
; PRIOR APPLICATION NUMBER: 60/188,786  
; PRIOR FILING DATE: 2000-03-13  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 8  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus type 1  
US-09-805-805-8

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Db 1 YGRKKRQRRR 11

## RESULT 6

US-09-821-821-24  
; Sequence 24, Application US/09821821  
; Patent No. US20020064823A1  
; GENERAL INFORMATION:  
; APPLICANT: Welcher, Andrew A.  
; APPLICANT: Calzone, Frank J.  
; TITLE OF INVENTION: CD20/IGe-Receptor Like Molecules and Uses Thereof  
; FILE REFERENCE: 01017/36938A  
; CURRENT APPLICATION NUMBER: US/09/821,821

; CURRENT FILING DATE: 2001-03-29  
; PRIOR APPLICATION NUMBER: US 09/723,258  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: US 60/193,728  
; PRIOR FILING DATE: 2000-03-30  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 24  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide  
US-09-821-821-24

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Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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Db 1 YGRKKRQRRR 11

RESULT 7  
US-09-895-943-13  
; Sequence 13, Application US/09895943  
; Patent No. US20020068323A1  
; GENERAL INFORMATION:  
; APPLICANT: Sarris, Chris  
; APPLICANT: Chang, Ming-Shi  
; TITLE OF INVENTION: Thymic Stromal Lymphopoietin Receptor Molecules and  
; TITLE OF INVENTION: Uses Thereof  
; FILE REFERENCE: 00-514-C  
; CURRENT APPLICATION NUMBER: US/09/895,943  
; CURRENT FILING DATE: 2001-06-28  
; PRIOR APPLICATION NUMBER: 60/214,866  
; PRIOR FILING DATE: 2000-06-28  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn Ver. 2.0  
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; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus type 1  
US-09-895-943-13

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Db 1 YGRKKRQRRR 11

RESULT 8  
US-09-825-414-91  
; Sequence 91, Application US/09825414  
; Patent No. US20020083489A1  
; GENERAL INFORMATION:  
; APPLICANT: Collmer, Alan  
; APPLICANT: Alfano, James R.  
; APPLICANT: Charkowski, Amy O.  
; TITLE OF INVENTION: DNA MOLECULES AND POLYPEPTIDES OF PSEUDOMONAS SYRINGAE  
; TITLE OF INVENTION: HRP PATHOGENICITY ISLAND AND THEIR USES  
; FILE REFERENCE: 19603/3243  
; CURRENT APPLICATION NUMBER: US/09/825,414  
; CURRENT FILING DATE: 2001-04-03  
; PRIOR APPLICATION NUMBER: 60/194,160  
; PRIOR FILING DATE: 2000-04-03  
; PRIOR APPLICATION NUMBER: 60/224,604  
; PRIOR FILING DATE: 2000-08-11  
; PRIOR APPLICATION NUMBER: 60/249,548

; PRIOR FILING DATE: 2000-11-17  
; NUMBER OF SEQ ID NOS: 91  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 91  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: human  
; OTHER INFORMATION: Immunodeficiency virus TAT protein, transduction  
; OTHER INFORMATION: domain  
US-09-825-414-91

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Best Local Similarity 100.0%; Pred. No. 0.018;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 YGRKKRQRRR 11  
Db 1 YGRKKRQRRR 11

RESULT 9  
US-09-867-274-23  
; Sequence 23, Application US/09867274  
; Patent No. US20020106650A1  
; GENERAL INFORMATION:  
; APPLICANT: Paszty, Christopher  
; APPLICANT: Gao, Yongming  
; TITLE OF INVENTION: Cysteine Knot Polypeptides: Cloaked-2 Molecules and Uses Thereof  
; FILE REFERENCE: 01017/37428  
; CURRENT APPLICATION NUMBER: US/09/867,274  
; CURRENT FILING DATE: 2001-05-29  
; PRIOR APPLICATION NUMBER: US 60/208,550  
; PRIOR FILING DATE: 2000-06-01  
; PRIOR APPLICATION NUMBER: US 60/223,542  
; PRIOR FILING DATE: 2000-08-04  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 23  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: HIV TAT peptide  
US-09-867-274-23

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RESULT 10  
US-09-955-866-24  
; Sequence 24, Application US/09955866  
; Patent No. US20020107363A1  
; GENERAL INFORMATION:  
; APPLICANT: Fox, Michael  
; APPLICANT: Sullivan, John K.  
; APPLICANT: Holst, Paige  
; APPLICANT: Yoshinaga, Steven Kiyoshi  
; TITLE OF INVENTION: B7-Like Polypeptides and Uses Thereof  
; FILE REFERENCE: 00,759-A  
; CURRENT APPLICATION NUMBER: US/09/955,866  
; CURRENT FILING DATE: 2001-09-19  
; PRIOR APPLICATION NUMBER: 60/233,867  
; PRIOR FILING DATE: 2000-09-20  
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US-09-955-866-24

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US-09-928-175-25
; Sequence 25, Application US/09928175
; Patent No. US20020123618A1
; GENERAL INFORMATION:
; APPLICANT: Paszty, Christopher J.
; APPLICANT: Gong, Jianhua
; APPLICANT: Daugherty, Betsy
; APPLICANT: Rogers, No. US20020123618Alma
; TITLE OF INVENTION: Leucine-Rich G Protein Coupled Receptor-8 Molecules and
; FILE REFERENCE: 00-1229
; CURRENT APPLICATION NUMBER: US/09/928,175
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/224,455
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
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; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-928-175-25

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Db      1 YGRKKRQRRR 11
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RESULT 12
US-09-995-542-13
; Sequence 13, Application US/09995542
; Patent No. US20020127647A1
; GENERAL INFORMATION:
; APPLICANT: Shutter, John
; APPLICANT: Ullas, Laarni
; TITLE OF INVENTION: ATP-Binding Cassette Transporter-Like Molecules and
; FILE REFERENCE: 00-658-A
; CURRENT APPLICATION NUMBER: US/09/995,542
; CURRENT FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: 60/253,520
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
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; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-995-542-13

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US-09-927-850-18
; Sequence 18, Application US/09927850
; Patent No. US20020137137A1
; GENERAL INFORMATION:
; APPLICANT: Welcher, Andrew
; APPLICANT: Wen, Duanzhi
; APPLICANT: Kelly, Michael
; TITLE OF INVENTION: Interferon-Like Molecules and Uses Thereof
; FILE REFERENCE: 99,372-F
; CURRENT APPLICATION NUMBER: US/09/927,850
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 09/724,860
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/169,720
; PRIOR FILING DATE: 1999-12-08
; NUMBER OF SEQ ID NOS: 39
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; Sequence 4, Application US/09984183
; Patent No. US20020142983A1
; GENERAL INFORMATION:
; APPLICANT: AGRAWAL, BABITA
; APPLICANT: LONGENECKER, MICHAEL B.
; TITLE OF INVENTION: MUC-1 ANTAGONISTS AND METHODS OF TREATING IMMUNE
; FILE REFERENCE: 042881/0130
; CURRENT APPLICATION NUMBER: US/09/984,183
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/457,354
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 60/111,973
; PRIOR FILING DATE: 1998-12-11
; NUMBER OF SEQ ID NOS: 30
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; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
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Db      1 YGRKKRQRRR 11
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RESULT 15



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; Patent No. US20020147145A1  
; GENERAL INFORMATION:  
; APPLICANT: Zealand Pharmaceuticals A/S  
; TITLE OF INVENTION: MATERIALS AND METHODS RELATING TO THE DEGRADATION OF Cdc25A IN RE  
; TITLE OF INVENTION: TO DNA DAMAGE  
; FILE REFERENCE: 55888 (45487)  
; CURRENT APPLICATION NUMBER: US/09/949,196  
; CURRENT FILING DATE: 2001-07-09  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn version 3.1  
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; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic peptide sequence  
US-09-949-196-15

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

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Title: US-10-049-822A-12

Perfect score: 58

Sequence: 1 YGRKKRQRRR 11

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#### SUMMARIES

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12	58	100.0	11	4	US-09-775-052A-2
13	58	100.0	11	4	US-09-911-842A-6
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23	58	100.0	12	1	US-08-450-246-47
24	58	100.0	12	1	US-08-450-098-47
25	58	100.0	12	1	US-08-451-233-47
26	58	100.0	12	1	US-08-450-236-47
27	58	100.0	12	2	US-08-733-505A-50

28 58 100.0 12 3 US-08-235-403-47 Sequence 47, Appl  
29 58 100.0 12 4 US-09-254-126D-46 Sequence 46, Appl  
30 58 100.0 12 4 US-09-656-121-14 Sequence 14, Appl  
31 58 100.0 12 4 US-09-656-121-15 Sequence 15, Appl  
32 58 100.0 14 5 PCT-US95-06077-4 Sequence 4, Appl  
33 58 100.0 14 5 PCT-US95-06077-10 Sequence 10, Appl  
34 58 100.0 14 5 PCT-US95-06077-11 Sequence 11, Appl  
35 58 100.0 14 5 PCT-US95-06077-12 Sequence 12, Appl  
36 58 100.0 15 1 US-08-450-257-5 Sequence 5, Appl  
37 58 100.0 15 1 US-08-450-246-5 Sequence 5, Appl  
38 58 100.0 15 1 US-08-450-246-6 Sequence 6, Appl  
39 58 100.0 15 1 US-08-450-098-5 Sequence 5, Appl  
40 58 100.0 15 1 US-08-450-098-6 Sequence 6, Appl  
41 58 100.0 15 1 US-08-451-233-5 Sequence 5, Appl  
42 58 100.0 15 1 US-08-451-233-6 Sequence 6, Appl  
43 58 100.0 15 1 US-08-450-236-5 Sequence 5, Appl  
44 58 100.0 15 1 US-08-450-236-6 Sequence 6, Appl  
45 58 100.0 15 1 US-08-450-236-6 Sequence 6, Appl

#### ALIGNMENTS

RESULT 1  
US-08-706-741B-54  
; Sequence 54, Application US/08706741B  
; Patent No. 5955593  
; GENERAL INFORMATION:  
; APPLICANT: KORSMEYER, STANLEY J.  
; TITLE OF INVENTION: BH3 INTERACTING DOMAIN DEATH AGONIST  
; NUMBER OF SEQUENCES: 88  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.  
; STREET: 7733 FORSYTH BLVD., SUITE 1400  
; CITY: ST. LOUIS  
; STATE: MISSOURI  
; COUNTRY: USA  
; ZIP: 63146  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/706,741B  
; FILING DATE: 09-SEP-1996  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: HOLLAND, DONALD R.  
; REGISTRATION NUMBER: 35,197  
; REFERENCE/DOCKET NUMBER: 965017  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314) 727-5188  
; TELEFAX: (314) 727-6092  
; INFORMATION FOR SEQ ID NO: 54:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-706-741B-54

Query Match 100.0%; Score 58; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 YGRKKRQRRR 11  
| | | | |  
Db 1 YGRKKRQRRR 11

RESULT 2

US-08-924-695A-54  
; Sequence 54, Application US/08924695A  
; Patent No. 598583  
; GENERAL INFORMATION:  
; APPLICANT: KORSMEYER, STANLEY J.  
; TITLE OF INVENTION: BH3 INTERACTING DOMAIN DEATH AGONIST  
; NUMBER OF SEQUENCES: 88  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HOWELL & HAFFERKAMP, L.C.  
; STREET: 7733 FORSYTH BLVD., SUITE 1400  
; CITY: ST. LOUIS  
; STATE: MISSOURI  
; COUNTRY: USA  
; ZIP: 63105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/924,695A  
; FILING DATE: 09-SEP-1997  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: HOLLAND, DONALD R.  
; REGISTRATION NUMBER: 35,197  
; REFERENCE/DOCKET NUMBER: 971798  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314) 727-5188  
; TELEFAX: (314) 727-6092  
; INFORMATION FOR SEQ ID NO: 54:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-924-695A-54

Query Match 100.0%; Score 58; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKKRRQRRR 11  
| | | | | | | | | |  
Db 1 YGRKKRRQRRR 11

RESULT 3  
US-09-208-966-2  
; Sequence 2, Application US/09208966  
; Patent No. 6221355  
; GENERAL INFORMATION:  
; APPLICANT: Dowdy, Steven F.  
; TITLE OF INVENTION: ANTI-PATHOGEN SYSTEM AND METHODS OF USE THEREOF  
; FILE REFERENCE: 48881/1742  
; CURRENT APPLICATION NUMBER: US/09/208,966  
; CURRENT FILING DATE: 1998-12-10  
; EARLIER APPLICATION NUMBER: 60/082,402  
; EARLIER FILING DATE: 1998-04-20  
; EARLIER APPLICATION NUMBER: 60/069,012  
; EARLIER FILING DATE: 1997-12-10  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: human  
US-09-208-966-2

Query Match 100.0%; Score 58; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKKRRQRRR 11  
| | | | | | | | | |  
Db 1 YGRKKRRQRRR 11  
  
RESULT 4  
US-09-296-089-37  
; Sequence 37, Application US/09296089  
; Patent No. 6303576  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Byers, Stephen  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING  
; TITLE OF INVENTION: BETA-CATENIN MEDIATED GENE EXPRESSION  
; FILE REFERENCE: 100086.411  
; CURRENT APPLICATION NUMBER: US/09/296,089  
; CURRENT FILING DATE: 1999-04-21  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 37  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus  
US-09-296-089-37

Query Match 100.0%; Score 58; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKKRRQRRR 11  
| | | | | | | | | |  
Db 1 YGRKKRRQRRR 11

RESULT 5  
US-09-837-863-2  
; Sequence 2, Application US/09837863  
; Patent No. 6468754  
; GENERAL INFORMATION:  
; APPLICANT: Greene, Amy  
; APPLICANT: Zhou, Hua  
; APPLICANT: Thode, Silke  
; APPLICANT: Jarnigan, Kurt  
; TITLE OF INVENTION: Vector and Method for Targeted Replacement and Disruption  
; TITLE OF INVENTION: of an Integrated DNA Sequence  
; FILE REFERENCE: 025.1US  
; CURRENT APPLICATION NUMBER: US/09/837,863  
; CURRENT FILING DATE: 2001-04-17  
; PRIOR APPLICATION NUMBER: US 60/198,498  
; PRIOR FILING DATE: 2000-04-18  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus  
US-09-837-863-2

Query Match 100.0%; Score 58; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKKRRQRRR 11  
| | | | | | | | | |  
Db 1 YGRKKRRQRRR 11

RESULT 6  
US-09-660-742-1  
; Sequence 1, Application US/09660742  
; Patent No. 6485977

; GENERAL INFORMATION:  
; APPLICANT: Collmer, Alan  
; APPLICANT: Beer, Steven V.  
; TITLE OF INVENTION: RECOMBINANT CONSTRUCTS AND TECHNIQUES FOR DELIVERING TO  
; TITLE OF INVENTION: EUCARYOTIC CELLS BACTERIAL PROTEINS THAT ARE SECRETED  
; TITLE OF INVENTION: VIA TYPE III SECRETION SYSTEMS  
; FILE REFERENCE: 19603/4021  
; CURRENT APPLICATION NUMBER: US/09/660,742  
; CURRENT FILING DATE: 2000-09-13  
; PRIOR APPLICATION NUMBER: 60/153,507  
; PRIOR FILING DATE: 1999-09-13  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-660-742-1

Query Match 100.0%; Score 58; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKKRQRRR 11  
| | | | | | | | | | | |  
Db 1 YGRKKRQRRR 11

RESULT 7  
US-09-434-345-2  
; Sequence 2, Application US/09434345  
; Patent No. 6511676  
; GENERAL INFORMATION:  
; APPLICANT: Boulikas, Teni  
; TITLE OF INVENTION: THERAPY FOR HUMAN CANCERS USING  
; TITLE OF INVENTION: CISPLATIN AND OTHER DRUGS OR GENES ENCAPSULATED INTO  
; TITLE OF INVENTION: LIPOSOMES  
; FILE REFERENCE: TB 2001.00  
; CURRENT APPLICATION NUMBER: US/09/434,345  
; CURRENT FILING DATE: 1999-11-05  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Human Immunodeficiency Virus  
US-09-434-345-2

Query Match 100.0%; Score 58; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKKRQRRR 11  
| | | | | | | | | | | |  
Db 1 YGRKKRQRRR 11

RESULT 8  
US-09-632-287A-22  
; Sequence 22, Application US/09632287A  
; Patent No. 6521422  
; GENERAL INFORMATION:  
; APPLICANT: Hsu, Hailing  
; APPLICANT: Wooden, Scott K  
; APPLICANT: Boyle, William J  
; TITLE OF INVENTION: Fhm, A No. 6521422el Member of the TNF Ligand Supergene Family  
; FILE REFERENCE: 01017/35550A  
; CURRENT APPLICATION NUMBER: US/09/632,287A  
; CURRENT FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: US 60/147,294  
; PRIOR FILING DATE: 1999-08-04  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 22  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide from the HIV TAT prot  
US-09-632-287A-22

Query Match 100.0%; Score 58; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKKRQRRR 11  
| | | | | | | | | | | |  
Db 1 YGRKKRQRRR 11

RESULT 9  
US-09-632-277A-4  
; Sequence 4, Application US/09632277A  
; Patent No. 6599716  
; GENERAL INFORMATION:  
; APPLICANT: Hsu, Hailing  
; TITLE OF INVENTION: NTR3 A No. 6599716el Member of the TNF-Receptor Supergene Family  
; FILE REFERENCE: 01017/3549A  
; CURRENT APPLICATION NUMBER: US/09/632,277A  
; CURRENT FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: US 60/147,297  
; PRIOR FILING DATE: 1999-08-04  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: HIV TAT peptide  
US-09-632-277A-4

Query Match 100.0%; Score 58; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKKRQRRR 11  
| | | | | | | | | | | |  
Db 1 YGRKKRQRRR 11

RESULT 10  
US-09-612-033B-15  
; Sequence 15, Application US/09612033B  
; Patent No. 6627199  
; GENERAL INFORMATION:  
; APPLICANT: Saris, Chris  
; TITLE OF INVENTION: Isolation, Identification, and Characterization of  
; TITLE OF INVENTION: tmst2, a No. 6627199el Member of the TNF-Receptor Superfamily  
; FILE REFERENCE: 01017/35434A  
; CURRENT APPLICATION NUMBER: US/09/612,033B  
; CURRENT FILING DATE: 2000-07-07  
; PRIOR APPLICATION NUMBER: US 60/143,063  
; PRIOR FILING DATE: 1999-07-09  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 15  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: peptide  
US-09-612-033B-15

Query Match 100.0%; Score 58; DB 4; Length 11;

Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKKRQRRR 11  
| | | | | | | | | |  
Db 1 YGRKKRQRRR 11

## RESULT 11

US-09-780-070-37  
; Sequence 37, Application US/09780070  
; Patent No. 6632616  
; GENERAL INFORMATION:  
; APPLICANT: Burke, James  
; APPLICANT: Strittmatter, Warren  
; APPLICANT: Nagai, Yoshitaka  
; TITLE OF INVENTION: COMPOUNDS THAT SELECTIVELY BIND TO EXPANDED POLYGLUTAMINE REPEAT  
; FILE REFERENCE: 5405.242  
; CURRENT APPLICATION NUMBER: US/09/780,070  
; CURRENT FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: 60/189,781  
; PRIOR FILING DATE: 2000-03-16  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 37  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus  
US-09-780-070-37

Query Match 100.0%; Score 58; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKKRQRRR 11  
| | | | | | | | | |  
Db 1 YGRKKRQRRR 11

## RESULT 12

US-09-775-052A-2  
; Sequence 2, Application US/09775052A  
; Patent No. 6645501  
; GENERAL INFORMATION:  
; APPLICANT: Dowdy, Steven F.  
; TITLE OF INVENTION: ANTI-PATHOGEN SYSTEM AND METHODS OF USE THEREOF  
; FILE REFERENCE: 48881/1742  
; CURRENT APPLICATION NUMBER: US/09/775,052A  
; CURRENT FILING DATE: 2001-12-05  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/208,966  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-10  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/069,012  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-12-10  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: human  
US-09-775-052A-2

Query Match 100.0%; Score 58; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKKRQRRR 11  
| | | | | | | | | |  
Db 1 YGRKKRQRRR 11

## RESULT 13

US-09-911-842A-6

; Sequence 6, Application US/09911842A  
; Patent No. 6656707  
; GENERAL INFORMATION:  
; APPLICANT: Amgen Inc.  
; TITLE OF INVENTION: C3B/C4B COMPLEMENT RECEPTOR-LIKE MOLECULES AND USES THEREOF  
; FILE REFERENCE: 01017/37592  
; CURRENT APPLICATION NUMBER: US/09/911,842A  
; CURRENT FILING DATE: 2001-07-24  
; PRIOR APPLICATION NUMBER: US 60/222,438  
; PRIOR FILING DATE: 2000-08-01  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 6  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-911-842A-6

Query Match 100.0%; Score 58; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKKRQRRR 11  
| | | | | | | | | |  
Db 1 YGRKKRQRRR 11

## RESULT 14

US-09-997-465B-2  
; Sequence 2, Application US/09997465B  
; Patent No. 6673574  
; GENERAL INFORMATION:  
; APPLICANT: Stern, William  
; APPLICANT: Mehta, No. 6673574er M.  
; APPLICANT: Ray, Martha V.L.  
; TITLE OF INVENTION: IMPROVED ORAL DELIVERY OF PEPTIDES USING ENZYME-CLEAVABLE MEMBRAN  
; FILE REFERENCE: P/546-247  
; CURRENT APPLICATION NUMBER: US/09/997,465B  
; CURRENT FILING DATE: 2001-11-29  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus type 1  
US-09-997-465B-2

Query Match 100.0%; Score 58; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKKRQRRR 11  
| | | | | | | | | |  
Db 1 YGRKKRQRRR 11

## RESULT 15

US-10-083-889-17  
; Sequence 17, Application US/10083889  
; Patent No. 6673894  
; GENERAL INFORMATION:  
; APPLICANT: Zahner, Joseph E.  
; TITLE OF INVENTION: Inhibitor of cell proliferation and methods of use thereof.  
; FILE REFERENCE: 16850-7331  
; CURRENT APPLICATION NUMBER: US/10/083,889  
; CURRENT FILING DATE: 2002-02-27  
; PRIOR APPLICATION NUMBER: US 60/271,798  
; PRIOR FILING DATE: 2001-02-27  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: Microsoft Word 97  
; SEQ ID NO 17  
; LENGTH: 11

; TYPE: PRT  
; ORGANISM: HIV-1  
US-10-083-889-17

Query Match 100.0%; Score 58; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKKRQRRR 11  
| | | | | | | | | |  
Db 1 YGRKKRQRRR 11

Search completed: March 31, 2005, 00:32:39  
Job time : 4.2 secs

Figure 1. The effect of the concentration of the *Agrobacterium* suspension on the transformation efficiency of *Agrobacterium* strains.



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 31, 2005, 00:17:06 ; Search time 7.7 Seconds  
(without alignments)  
552.515 Million cell updates/sec

Title: US-10-049-822A-12

Perfect score: 58

Sequence: 1 YGRKRRQRRR 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

- 1: Geneseqp1980s:\*
- 2: Geneseqp1990s:\*
- 3: Geneseqp2000s:\*
- 4: Geneseqp2001s:\*
- 5: Geneseqp2002s:\*
- 6: Geneseqp2003as:\*
- 7: Geneseqp2003bs:\*
- 8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58	100.0	11	2	AAW50263 HIV-1 tat
2	58	100.0	11	2	AAY05415 Tat pepti
3	58	100.0	11	2	AAY25075 TAT trans
4	58	100.0	11	3	AAB27088 Beta-cate
5	58	100.0	11	3	AB09907 HIV tat p
6	58	100.0	11	3	AAY93542 Amino aci
7	58	100.0	11	3	AAY71015 Human imm
8	58	100.0	11	3	AAB35698 Peptide a
9	58	100.0	11	3	AB033961 Minimal e
10	58	100.0	11	3	AAB29413 HIV TAT t
11	58	100.0	11	3	AB03332 TAT prote
12	58	100.0	11	4	AB71757 HIV TAT p
13	58	100.0	11	4	AB71756 NTR3 deri
14	58	100.0	11	4	AB60006 Internali
15	58	100.0	11	4	AAB05268 Human imm
16	58	100.0	11	4	AAE02973 Protein t
17	58	100.0	11	4	AAE03418 Human imm
18	58	100.0	11	4	AAE03815 HIV tat p
19	58	100.0	11	4	AB98683 HIV TAT p
20	58	100.0	11	4	AB73305 HIV-1 TAT
21	58	100.0	11	4	AG70458 Human G2
22	58	100.0	11	4	AG68376 Human Chk
23	58	100.0	11	4	AG65673 HIV tat p
24	58	100.0	11	4	AAE12605 Human imm
25	58	100.0	11	4	AAB67673 Transduct

#### ALIGNMENTS

##### RESULT 1

AAW50263  
ID AAW50263 standard; protein; 11 AA.  
XX  
AC AAW50263;  
XX  
DT 17-OCT-2003 (revised)  
DT 20-JUL-1998 (first entry)  
XX  
DS HIV-1 tat protein.  
XX  
KW Mouse; BH3 interacting domain death agonist; BID; BCL-2 family;  
KW apoptosis; regulation; cell death; inflammation; cancer; arthritis;  
KW autoimmune disease; viral infection; lymphoproliferative.  
XX  
OS Human immunodeficiency virus 1.  
XX  
FN WO9809980-A1.  
XX  
PD 12-MAR-1998.  
XX  
PF 09-SEP-1997; 97WO-US015872.  
XX  
PR 09-SEP-1996; 96US-00706741.  
XX  
(UNIW ) UNIV WASHINGTON.  
PI Korsmeyer SJ;  
XX  
WPI; 1998-193546/17.  
XX  
BH3 interacting domain death agonist polypeptide - used for treating  
decreased apoptotic conditions resulting from inflammation etc.  
XX  
Example 8; Page 85; 118pp; English.

The present sequence represents the HIV-1 tat protein which is used in an example of the present invention which describes a BH3 interacting domain death agonist (BID) truncated protein. The BID protein, the DNA encoding it or antisense sequences can be used for preventing or treating a decreased apoptotic state of a cell. The decreased apoptotic state that is treated results from a disease such as cancer, viral infections, lymphoproliferative conditions, arthritis, inflammation and autoimmune diseases. Antibodies against the BID protein can be used for detecting a BID polypeptide in a cell or population of cell. The nucleic acid sequence and the BID protein can also be used for treating immunodeficiency disease (including AIDS), senescence, neurodegenerative disease, ischaemic and reperfusion cell death, infertility and wound-

CC healing. Primers derived from the nucleic acid encoding the BID protein  
CC can be used for detecting/quantitating the protein and for detecting  
CC alterations in the nucleic acid encoding the BID protein. (Updated on 17-  
CC OCT-2003 to standardise OS field)

XX  
SQ Sequence 11 AA;

Query Match 100.0%; Score 58; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.013;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKKRQRRR 11  
| | | | | | | | | |  
Db 1 YGRKKRQRRR 11

RESULT 2  
AA05415  
ID AAY05415 standard; peptide; 11 AA.

XX  
AC AAY05415;

DT 02-JUL-1999 (first entry)

DE Tat peptide.

XX BH3 domain; cell death agonist; bcl homology domain; BCL-2 family;  
KW apoptosis promoter; cancer cell; virus infected cell; inflammation;  
KW autoantibody producing cell; cancer; lymphoproliferative condition;  
KW arthritis; autoimmune disease; therapy.

XX Unidentified.

PN WO9916787-A1.

XX 08-APR-1999.

XX 22-SEP-1998; 98WO-US019765.

PR 26-SEP-1997; 97US-0060133P.

PR 07-OCT-1997; 97US-00946039.

XX (UNIW ) UNIV WASHINGTON.

PI Koremeyer SJ;

DR WPI; 1999-255058/21.

XX Bcl homology domain 3 polypeptide.

XX Claim 7; Page 67; 104pp; English.

XX This sequence represents a Tat peptide. The invention relates to a bcl  
CC homology domain 3 (BH3 domain), derived from a proapoptotic member of the  
CC BCL-2 family. The BH3 polypeptide can be used in a method for promoting  
CC apoptosis in a target cell, especially where the cell is a cancer cell a  
CC virus infected cell or an autoantibody producing cell. The BH3  
CC polypeptide can be used in therapeutic compositions for treating disease  
CC including cancer, other lymphoproliferative conditions, arthritis,  
CC inflammation, and autoimmune diseases, which may result from the down  
CC regulation of cell death regulation

XX Sequence 11 AA;

Query Match 100.0%; Score 58; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.013;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKKRQRRR 11  
| | | | | | | | | |  
Db 1 YGRKKRQRRR 11

RESULT 3  
AAY25075

ID AAY25075 standard; peptide; 11 AA.

XX  
AC AAY25075;

DT 24-AUG-1999 (first entry)

DE Tat transduction domain peptide motif.

XX Anti-pathogen; fusion protein; protein transduction domain; PTD; AZT;  
KW cytotoxic domain; suppressor; infection; medicament; ddi; ddc; d4T; 3TC;  
KW PTC; DAPD; 1592U89; CS92; acyclovir; ganciclovir; peniclovir; interferon;  
KW apoptosis; virus; HIV; cytomegalovirus; CMV; herpes simplex virus; HSV-1;  
KW hepatitis virus; Kaposi's sarcoma-associated herpes virus; KSHV;  
KW herpes virus; yellow fever virus; flavivirus; rhinovirus; plasmodial;  
KW transduction efficiency; cytotoxin.

XX Unidentified.

XX WO9929721-A1.

XX 17-JUN-1999.

XX 10-DEC-1998; 98WO-US026358.

PR 10-DEC-1997; 97US-0069012P.

PR 20-APR-1998; 98US-0082402P.

XX (UNIW ) UNIV WASHINGTON.

XX Dowdy SF;

XX WPI; 1999-394958/33.

XX New anti-pathogen systems, particularly for virus and plasmodium  
PT infections.

XX Claim 65; Page 34; 123pp; English.

XX This invention describes a novel anti-pathogen system (APS) comprising a  
CC fusion protein constructed from a covalently linked protein transduction  
CC domain (PTD) and a cytotoxic domain. The APS can be used for suppressing  
CC a pathogen infection in a mammal. The method may further comprise  
CC administering a medicament e.g. AZT, ddi, ddc, d4T, 3TC, FTC, DAPD,  
CC 1592U89, CS92, acyclovir, ganciclovir, peniclovir or an interferon. The  
CC APS can also be administered to a mammal in the presence of a pathogen to  
CC induce apoptosis in a predetermined population of cells. The products can  
CC be used for treating mammals suffering from or susceptible to a viral  
CC infection or a disease associated with a virus, e.g. HIV, cytomegalovirus  
CC (CMV), herpes simplex virus, e.g. type 1 (HSV-1) hepatitis virus, type C  
CC (HCV), Kaposi's sarcoma-associated herpes virus (KSHV or human herpes  
CC virus 8), yellow fever virus, flavivirus or rhinovirus, or suffering from  
CC or susceptible to plasmodial infection or a disease associated with a  
CC malarial infection, e.g. P. falciparum, P. vivax, P. ovale, or P.  
CC malariae. The APS exhibits high transduction efficiency and specifically  
CC kills or injures cells infected by one or more pathogens. Formation of  
CC the cytotoxin is minimized or eliminated in uninfected cells and in  
CC infected cells that keep the pathogen inactive. The APS can be  
CC specifically tailored to kill or injure cells infected by one or more  
CC pathogen strains. This sequence represents a Tat transduction domain  
CC peptide motif which is used in the method of the invention

XX Sequence 11 AA;

Query Match 100.0%; Score 58; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.013;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKKRQRRR 11  
| | | | | | | | | |  
Db 1 YGRKKRQRRR 11

RESULT 4  
 ID AAB27088 standard; peptide; 11 AA.  
 AC AAB27088;  
 DT 15-FEB-2001 (first entry)  
 DE Beta-catenin derived internalisation moiety SEQ ID NO: 75.  
 KW Beta-catenin; cadherin-mediated intercellular adhesion;  
 cell differentiation; modulating agent; hair loss; skin exfoliation;  
 internalisation moiety; flanking sequence; transcription; hearing loss.  
 KW KW  
 XX OS  
 XX OS Human immunodeficiency virus.  
 FN WO200053632-A1.  
 XX 14-SEP-2000.  
 PD 07-MAR-2000; 2000WO-CA000222.  
 XX 09-MAR-1999; 99US-00265107.  
 XX (UYMC-) UNIV MCGILL.  
 PA Blaschuk OW, Gour BJ;  
 PI WPI; 2000-594308/56.  
 DR Stimulating beta-catenin mediated gene expression, cellular  
 PT differentiation and hair growth, involves contacting cells with  
 PT modulating agent capable of inhibiting interaction between alpha and beta  
 PT catenin.  
 XX Disclosure; Page 19; 77pp; English.  
 XX The present invention is concerned with methods of modulating the amount  
 of free beta-catenin in the cell, and methods of stimulating the  
 expression of genes involved in cellular differentiation, the  
 transcription of which is under the control of beta-catenin. The peptides  
 given in AAB27053-B27088, AAB27284-B27300 and AAB27330-B27351 can be used  
 as modulating agents which interrupt the interaction between alpha and  
 beta catenin, causing increased levels of the latter and stimulating the  
 activation of beta-catenin mediated transcription. This can be used to  
 stimulate cell differentiation, which can then be used to promote hair  
 growth and skin exfoliation. This latter is particularly useful in the  
 improvement of photodamaged skin and to minimise wrinkles. The modulating  
 peptide can also be used to reduce hearing loss resulting from inner ear  
 disorders such as hyperacusis and tinnitus

KW Targeting signal; MUC-1; immunosuppression; autoimmune disorder;  
 KW immune disorder; inflammatory disorder.  
 XX OS  
 XX OS Human immunodeficiency virus.  
 FN WO200034468-A2.  
 XX 15-JUN-2000.  
 PD 09-DEC-1999; 99WO-US029016.  
 XX 11-DEC-1998; 98US-0111973P.  
 PR (BIOM-) BIOMIRA INC.  
 PA Agrawal B, Longenecker BM;  
 PI WPI; 2000-423418/36.  
 DR Use of agent capable of intracellularly inhibiting mucin MUC-1 for  
 XX inducing T-cell-based immunosuppression and for treating autoimmune  
 XX disorders, transplant rejection and inflammatory disorders.  
 PS Disclosure; Page 15; 51pp; English.  
 XX The present sequence is the tat protein transduction domain from HIV,  
 CC which can be used as a targeting signal. It can be used to internalise  
 CC sequences, such as MUC-1 antagonists, within the cell. MUC-1 is a  
 CC immunosuppressor, and antagonists act to reduce overactive immune  
 CC responses. Thus, the peptide can be used to treat inflammatory disorders  
 CC such as rheumatoid arthritis, psoriasis, allergic contact dermatitis and  
 CC ankylosing spondylitis, autoimmune disorders including myasthenia gravis,  
 CC systemic lupus erythematosus, polyarteritis nodosa, Goodpastures  
 CC syndrome, isopathic thrombocytopenic purpura, autoimmune haemolytic  
 CC anaemia, Graves' disease, rheumatic fever, pernicious anaemia, insulin-  
 CC resistant diabetes mellitus, bullous pemphigoid, pemphigus vulgaris,  
 CC viral myocarditis, autoimmune thyroiditis, male infertility, sarcoidosis,  
 CC allergic encephalomyelitis, multiple sclerosis, Sjorgens disease,  
 CC Reiter's disease, Celiac disease, sympathetic ophthalmia and primary  
 CC biliary cirrhosis, immune disorders, graft versus host disease and  
 CC transplant rejection  
 XX Sequence 11 AA;  
 SQ Query Match 100.0%; Score 58; DB 3; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 0.013;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YGRKKRRQRRR 11  
 DB 1 YGRKKRRQRRR 11  
 RESULT 6  
 AAB93542  
 ID AAB93542 standard; peptide; 11 AA.  
 XX AC AAB93542;  
 XX 25-SEP-2000 (first entry)  
 DT Amino acid sequence of a synthetic protein transduction domain.  
 DE Protein transduction system; protein transduction domain;  
 KW cytotoxic domain; pathogen infection; retroviral infection;  
 KW plasmidial infection; cancer; prostate cancer.  
 XX OS Synthetic.  
 XX WO200034308-A2.  
 FN 15-JUN-2000.  
 XX

PF 10-DEC-1999; 99WO-US029289.  
PR 10-DEC-1998; 98US-0111701P.  
XX (UNIW ) UNIV WASHINGTON.  
PA Dowdy SF;  
XX WPI; 2000-431269/37.  
XX Protein transduction system for treating cancer and pathogenic infections  
PT has a fusion protein comprising a protein transduction domain covalently  
PT linked to a cytotoxic domain.  
XX Example 10; Page 71; 127pp; English.  
XX AAY93542-51 represent synthetic protein transduction domains, which are  
CC used in the protein transduction system of the invention. The  
CC specification describes a protein transduction system, which comprises a  
CC fusion protein. This fusion protein has a covalently linked protein  
CC transduction domain and cytotoxic domain. The system is useful for  
CC treating pathogen infection in mammals, infections such as those caused  
CC by CMV, HSV-1, HCV, KSHV, yellow fever virus, flavivirus or rhinovirus,  
CC retroviral infections such as HIV-1, HIV-2, HTLV-3 and/or LAV, plasmoidal  
CC infections associated with P.faciapum, P.vivax, P.ovale, P.malariae. It  
CC is also useful for treating cancer, especially prostate cancer  
XX Sequence 11 AA;  
SQ

Query Match 100.0%; Score 58; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.013;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 YGRKKRQRRR 11  
Db 1 YGRKKRQRRR 11

RESULT 7  
AAY71015  
ID AAY71015 standard; peptide; 11 AA.  
XX AAY71015;  
XX 29-AUG-2000 (first entry)  
DE Human immunodeficiency virus TAT peptide.  
XX Phospholamban; PLB; sarcoplasmic reticulum Ca 2+ ATPase; SERCA2a; HIV;  
KW TAT protein; penestratin; transport peptide; cardiomyocyte; inhibitor;  
KW cargo peptide; contractilin; cardiac contractility; cardiac; treatment;  
KW cardiac disease; heart failure; myocardial dysfunction.  
XX Human immunodeficiency virus.  
OS WO200025804-A2.  
PN 11-MAY-2000.  
XX 02-NOV-1999; 99WO-US025692.  
XX 02-NOV-1998; 98US-0106718P.  
PR 27-JUL-1999; 99US-0145883P.  
XX (REGC ) UNIV CALIFORNIA.  
XX Chien K, Dillman W, Minamisawa S, He H, Hoshijima M, Meyer M;  
PI Scott C, Wang Y, Silverman GJ;  
XX WPI; 2000-365393/31.  
XX Treating cardiac diseases, e.g. heart failure or myocardial dysfunction  
PT comprises enhancing cardiac contractility by inhibiting interaction

PT between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine  
PT triphosphatase.  
XX Example 5; Page 54; 56pp; English.  
XX The patent discloses a method for the treatment of heart failure, using  
CC small peptide complexes and recombinant proteins, that induces  
CC phospholamban (PLB) deficiency and inhibits the interaction between PLB  
CC and sarcoplasmic reticulum Ca 2+ ATPase (SERCA2a) within cardiomyocytes.  
CC The peptide complex comprises of transport peptide like penetratin and  
CC cargo peptide selected from mutant PLB, native PLB or antibody against  
CC PLB protein (contractilin). Penetratin-PLB peptide functions as a  
CC dominant negative inhibitor of PLB-SERCA2a interaction, enhances cardiac  
CC contractility and reduces blood pressure. This method is useful for the  
CC treatment of cardiac disease e.g. heart failure and myocardial  
CC dysfunction. The present sequence is the amino terminal, 11-amino acid  
CC protein transduction domain of the denatured human immunodeficiency virus  
CC (HIV) TAT protein. It belongs to the penetratin class of peptides, with  
CC translocating properties having the ability to carry hydrophilic  
CC compounds across the plasma membrane. It is used in the construction of  
CC recombinant PLB peptides (e.g., TAT-PLB)  
XX Sequence 11 AA;  
SQ

Query Match 100.0%; Score 58; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.013;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 YGRKKRQRRR 11  
Db 1 YGRKKRQRRR 11

RESULT 8  
AAB35698  
ID AAB35698 standard; peptide; 11 AA.  
XX AAB35698;  
XX 12-SEP-2003 (revised)  
DT 16-FEB-2001 (first entry)  
XX Peptide associated with modified beta-catenin expression #31.  
DE Beta-catenin; cell differentiation; hair growth; cancer;  
KW Alzheimer's disease.  
XX Human immunodeficiency virus 1.  
OS WO200063246-A2.  
PN 26-OCT-2000.  
XX 21-APR-2000; 2000WO-US010753.  
XX 21-APR-1999; 99US-00296089.  
PR (ADHE-) ADHEREX TECHNOLOGIES INC.  
XX Blaschuk OW, Byers S, Gour BJ;  
PI WPI; 2000-679589/66.  
XX Use of modulating agent comprising internalization moiety and a peptide,  
PT for modulating beta-catenin mediated gene transcription and cell  
PT differentiation, for treating cancer, and for inhibiting Alzheimer's  
PT disease.  
XX Claim 6; Page 26; 47pp; English.  
XX The present invention relates to a method for modulating beta-catenin  
CC mediated gene transcription in a cell. The method involves contacting a  
CC cell with a modulating agent comprising an internalization moiety and a

CC peptide comprising a sequence LXXLL or peptide analogue of LXXLL. The  
CC method is useful for modulating beta-catenin mediated gene transcription,  
CC cell differentiation, hair growth, and retinoic acid activity, for  
CC treating cancer, and for inhibiting the development of Alzheimer's  
CC disease. (Updated on 12-SEP-2003 to standardise OS field)

XX Sequence 11 AA;

Query Match 100.0%; Score 58; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.013;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKKRQRRR 11  
| | | | | | | | | |  
Db 1 YGRKKRQRRR 11

#### RESULT 9

AAB03961  
ID AAB03961 standard; peptide; 11 AA.

XX AAB03961;

XX 26-FEB-2001 (first entry)

XX Minimal eleven amino acids present in PTAT.

XX Chimeric protein; fusion protein; FLICE like inhibitor protein; FLIP;  
KW Fas; TNF; apoptosis; caspase-8; ligand; T cell; thymocyte;  
KW tumour specific antigen; immune response; therapy; prophylaxis;  
KW diagnosis; HIV; human immunodeficiency syndrome; AIDS;  
KW acquired immune deficiency syndrome.

XX Human immunodeficiency virus.

OS WO200059935-A1.

XX 12-OCT-2000.

XX 05-APR-2000; 2000WO-US009002.

XX 05-APR-1999; 99US-0127867P.

XX 06-APR-1999; 99US-0128021P.

XX (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.

PA (PAYA/) PAYA C.

PA (ALGE/) ALGECIRAS-SCHMINICH A.

XX Paya C, Algeciras-Schminich A;

XX WPI; 2000-664988/64.

XX Fusion polypeptide useful for inhibiting ligand-induced apoptosis,  
PT comprises portion of anti-apoptotic polypeptide linked to a transport  
PT group.

PS Disclosure; Page 30; 89pp; English.

XX A chimeric group or fusion peptide which comprises a portion of an anti-  
CC apoptotic polypeptide which inhibits apoptosis of lymphocytes in  
CC combination with a transport group is described. The transport group is  
CC capable of transporting the chimeric group or fusion peptide across the  
CC cell membrane. The anti-apoptotic polypeptide is FLICE-like inhibitor  
CC protein (FLIP) which inhibits Fas and TNF mediated apoptosis by  
CC inhibiting binding of Caspase-8 to the Fas receptor complex, thus  
CC shutting off the downstream Fas signalling pathway. The chimeric group  
CC and fusion peptide are useful for inhibiting ligand-induced apoptosis by  
CC bringing them into contact with T cells. The chimeric group is useful for  
CC expanding T cells in vitro e.g. T cells specific for particular antigens  
CC such as tumour-specific antigen, for enhancing immune response and to  
CC inhibit the apoptosis of chronically activated T cells e.g. activated  
CC CD4<sup>+</sup> T cells in HIV infected patients. The chimeric group is also useful  
CC for therapeutic, prophylactic or diagnosis of intracellular delivery of

CC small molecules and macromolecules such as anti-apoptotic polypeptides  
CC and nucleic acids encoding such polypeptides. Two primers (AAA54297,  
CC AAA54298) were used to amplify the FLIP cDNA for subcloning into the XhoI  
CC -NcoI site of the pHA-TAT vector which contains the N-terminal protein  
CC transduction domain from the human immunodeficiency virus tat protein.  
CC Tat is a preferred transport moiety

XX Sequence 11 AA;

Query Match 100.0%; Score 58; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.013;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKKRQRRR 11  
| | | | | | | | | |  
Db 1 YGRKKRQRRR 11

#### RESULT 10

AAB29413  
ID AAB29413 standard; peptide; 11 AA.

XX AAB29413;

XX 09-FEB-2001 (first entry)

XX HIV TAT transduction domain, SEQ ID NO:2.

XX Protein transduction domain; fusion molecule; therapeutic agent;  
KW drug targeting; drug discovery; cell transduction; bioavailability;  
KW vaccine; nervous system disorder; Alzheimer's disease;  
KW Parkinson's disease; Huntington's disease; pre-senile dementia; epilepsy;  
KW seizure; compulsive behaviour; meningitis; encephalitis; ischaemia;  
KW spongiform encephalopathy; dyslexia; age-related memory loss;  
KW Lou Gehring's disease; viral infection; HIV; bacterial infection.

XX Human immunodeficiency virus.

OS WO200062067-A1.

XX 19-OCT-2000.

XX 28-FEB-2000; 2000WO-US005097.

XX 28-FEB-1999; 99US-0122757P.

XX 29-AUG-1999; 99US-0151291P.

XX (UNIW ) UNIV WASHINGTON.

XX Dowdy SF;

XX WPI; 2000-647439/62.

XX Fusion molecules comprising protein transduction domains and therapeutic  
PT agents, useful for treating e.g. Alzheimer's and Parkinson's diseases,  
PT dementia and epilepsy.

PS Disclosure; Page 50; 191pp; English.

XX The invention relates to a novel fusion molecule comprising at least one  
CC protein transduction domain (PTD) and at least one linked molecule, where  
CC the linked molecule has therapeutic or prophylactic activity against a  
CC medical condition. The invention also relates to methods of drug  
CC discovery in which the test compound is linked to a suitable transducing  
CC protein and introduced to a cell; a method of killing resistant  
CC microorganisms using a suitable fusion molecule; a mammal comprising a  
CC covalently linked fusion molecule; and a mammal adapted for experimental  
CC use in which at least one transduction molecule has been transduced into  
CC essentially all the cells of the mammal. The fusion molecule is used to  
CC deliver a therapeutic agent to a mammal, especially a human. The linked  
CC molecule may be a vaccine, an anti-infective drug, a cardiovascular drug,  
CC an antitumour drug, an analgesic, an anti-inflammatory, a diagnostic  
CC marker or a drug for the treatment or prevention of a central or

CC peripheral nervous system disorder. The central nervous system (CNS)  
 CC disorder is especially Alzheimer's disease, Parkinson's disease,  
 CC Huntington's disease, and also includes pre-senile dementia, epilepsy and  
 CC seizures, compulsive behaviour, meningitis (including viral and bacterial  
 CC meningitis), encephalitis, ischaemia, scrapie (or related spongiform  
 CC encephalopathies), dyslexia, age-related memory loss or Lou Gehring's  
 CC disease. Fusion molecules can also be used to kill virally infected  
 CC cells, especially those infected with HIV. The vaccines are used to treat  
 CC or prevent bacterial or viral infections. The methods are a highly  
 CC effective means for transducing a molecule into an entire mammal or into  
 CC specific cells, tissues, organs and systems within it. They also overcome  
 CC bioavailability problems that are associated with many therapeutic agents  
 CC (e.g., large molecular size, hydrophobicity, hydrophilicity, biological  
 CC resistance), by providing efficient transduction of the target cell. The  
 CC present sequence represents a protein transduction domain used in the  
 CC invention

XX  
 SQ Sequence 11 AA;

Query Match 100.0%; Score 58; DB 3; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 0.013;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKKRQRRR 11  
 |||||  
 Db 1 YGRKKRQRRR 11

RESULT 11  
 AAB03932  
 ID AAB03932 standard; peptide; 11 AA.  
 AC AAB03932;  
 XX  
 DT 12-SEP-2003 (revised)  
 DT 26-FEB-2001 (first entry)  
 XX  
 DE TAT protein transduction domain (internalisation moiety).  
 XX  
 KW Modulating agent; beta-catenin; hair loss; hair growth; skin;  
 KW exfoliation; Alzheimer's disease; gene transcription;  
 KW cell differentiation; hearing loss; inner ear; hyperacusis; tinnitus;  
 KW hair regeneration.  
 XX  
 OS Human immunodeficiency virus; (HIV).  
 XX  
 PN WO20005939-A1.  
 XX  
 PD 12-OCT-2000.  
 XX  
 PF 04-APR-2000; 2000WO-US009174.  
 XX  
 PR 05-APR-1999; 99US-00288373.  
 XX  
 PA (ADHE-) ADHEREX TECHNOLOGIES INC.  
 XX  
 PI Blaschuk OW, Byers S, Gour BJ;  
 XX  
 DR WPI; 2000-679355/66.  
 XX  
 PT Modulating agents for inhibiting degradation of cytoplasmic beta-catenin,  
 PT used for e.g. stimulating hair growth or reducing hair loss, inhibiting  
 PT development of Alzheimer's disease, comprise internalization moiety and  
 PT amino acid sequence.  
 XX  
 PS Claim 4; Page 46; 49pp; English.  
 XX  
 CC Modulating agents for inhibiting degradation of cytoplasmic beta-catenin  
 CC are described. The modulating agent comprises an internalisation moiety  
 CC and one or more of an amino acid sequence SYDS(PO.4)GIHS(PO.4)G, or a  
 CC peptide analogue or peptidomimetic of the amino acid sequence. The  
 CC modulating agents are useful for the manufacture of a medicament for  
 CC stimulating hair growth or reducing hair loss, stimulating skin

CC exfoliation, and inhibiting the development of Alzheimer's disease. They  
 CC may also be used to increase the beta-catenin level in a cell, to  
 CC stimulate activation of gene transcription in a cell, and to stimulate  
 CC cell differentiation. They may further be used to ameliorate hearing loss  
 CC resulting from a variety of inner ear disorders, such as hyperacusis and  
 CC tinnitus, through regeneration of hair cells of the inner ear. (Updated  
 CC on 12-SEP-2003 to standardise OS field)

XX  
 SQ Sequence 11 AA;

Query Match 100.0%; Score 58; DB 3; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 0.013;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKKRQRRR 11  
 |||||  
 Db 1 YGRKKRQRRR 11

RESULT 12  
 AAB71757  
 ID AAB71757 standard; protein; 11 AA.  
 XX  
 AC AAB71757;  
 XX  
 DT 02-MAY-2001 (first entry)  
 XX  
 DE HIV TAT protein transduction domain.  
 XX  
 KW HIV; human immunodeficiency virus; protein transduction domain; NTR3;  
 KW tumour necrosis factor receptor; TNF receptor; anti-HIV; antianaemic;  
 KW immunosuppressive; antidiabetic; antiviral; antibacterial; cytostatic;  
 KW neuroprotective; antiinflammatory; anorectic; vasotropic; antirheumatoid;  
 KW antiarthritic; cerebroprotective; tuberculostatic; gene therapy; cancer;  
 KW blood disorder; brain disorder; autoimmune disease; infection.  
 XX  
 OS Human immunodeficiency virus.  
 XX  
 PN WO200110908-A1.  
 XX  
 PD 15-FEB-2001.  
 XX  
 PF 02-AUG-2000; 2000WO-US021287.  
 XX  
 PR 04-AUG-1999; 99US-0147297P.  
 XX  
 PA (AMGE-) AMGEN INC.  
 XX  
 PI Hsu H;  
 XX  
 DR WPI; 2001-191521/19.  
 XX  
 PT New tumor necrosis factor receptor, NTR3, useful for treating cancers,  
 PT stroke, anemia, obesity, rheumatoid arthritis and transplantation  
 PT rejection.  
 XX  
 PS Disclosure; Page 85; 135pp; English.  
 XX  
 CC The present sequence can be used to internalise proteins into a cell by  
 CC targeting the lipid bi-layer component of the cell membrane. The sequence  
 CC may be fused to an NTR3 antagonist and administered intracellularly to  
 CC inhibit the activity of the NTR3 molecule. NTR3 is a tumour necrosis  
 CC factor (TNF) receptor. NTR3 polynucleotides and polypeptides are useful  
 CC for treating diseases such as acquired-immunodeficiency syndrome (AIDS),  
 CC anaemia, autoimmune diseases, cachexia, cancer, cerebral malaria,  
 CC sick syndrome, haemorrhagic shock, hepatitis, insulin resistance,  
 CC leprosy, leukaemia, meningitis, multiple sclerosis, myocardial ischaemia,  
 CC obesity, rejection of transplanted organs, rheumatoid arthritis, septic  
 CC shock syndrome, stroke, adult respiratory distress syndrome (ARDS),  
 CC tuberculosis, and a number of viral diseases. The NTR3 polypeptide is  
 CC useful for identifying or developing new (ant)agonists of NTR3. It may be  
 CC used as an immunogen to which antibodies may be raised. NTR3 nucleic acid

CC molecules may be useful as hybridisation probes in diagnostic assays to  
CC test, either qualitatively or quantitatively, for the presence of an NTR3  
CC DNA or corresponding RNA in mammalian tissue or bodily fluid samples  
SQ Sequence 11 AA;

Query Match 100.0%; Score 58; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.013;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRKKRRQRRR 11  
| | | | | | | | | |  
DB 1 YGRKKRRQRRR 11

RESULT 13  
AAB71756  
ID AAB71756 standard; protein; 11 AA.

XX AAB71756;

AC AAB71756;

DT 02-MAY-2001 (first entry)

DE NTR3 derived peptide.

XX Human; NTR3; tumour necrosis factor receptor; TNF receptor; anti-HIV;  
KW antianaemic; immunosuppressive; antidiabetic; antiviral; antibacterial;  
KW cytoskeletal; neuroprotective; antiinflammatory; anorectic; vasotropic;  
KW antirheumatoid; antithyroid; cerebroprotective; tuberculostatic;  
KW gene therapy; cancer; blood disorder; brain disorder; autoimmune disease;  
KW infection.

XX Synthetic.

XX WO200110908-A1.

XX 15-FEB-2001.

XX 02-AUG-2000; 2000WO-US021287.

XX 04-AUG-1999; 99US-0147297P.

XX (AMGE-) AMGEN INC.

XX Hsu H;

XX WPI; 2001-191521/19.

XX New tumor necrosis factor receptor, NTR3, useful for treating cancers,  
PT stroke, anemia, obesity, rheumatoid arthritis and transplantation  
PT rejection.

PS Disclosure; Page 131; 135pp; English.

XX The present sequence is a peptide within which conservative and non-  
CC conservative amino acid substitutions may be made to generate analogues  
CC of the tumour necrosis factor (TNF) receptor polypeptide NTR3. NTR3  
CC polynucleotides and polypeptides are useful for treating diseases such as  
CC acquired-immunodeficiency syndrome (AIDS), anaemia, autoimmune diseases,  
CC cachexia, cancer, cerebral malaria, diabetes mellitus, disseminated  
CC intravascular coagulopathy, erythroid sick syndrome, haemorrhagic shock,  
CC hepatitis, insulin resistance, leprosy, leukaemia, meningitis, multiple  
CC sclerosis, myocardial ischaemia, obesity, rejection of transplanted  
CC organs, rheumatoid arthritis, septic shock syndrome, stroke, adult  
CC respiratory distress syndrome (ARDS), tuberculosis, and a number of viral  
CC diseases. The NTR3 polypeptide is useful for identifying or developing  
CC new (ant)agonists of NTR3. It may be used as an immunogen to which  
CC antibodies may be raised. NTR3 nucleic acid molecules may be useful as  
CC hybridisation probes in diagnostic assays to test, either qualitatively  
CC or quantitatively, for the presence of an NTR3 DNA or corresponding RNA  
CC in mammalian tissue or bodily fluid samples

XX Sequence 11 AA;

Query Match 100.0%; Score 58; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.013;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRKKRRQRRR 11  
| | | | | | | | | |  
DB 1 YGRKKRRQRRR 11

RESULT 14  
AAB60006  
ID AAB60006 standard; peptide; 11 AA.

XX AAB60006;

DT 05-NOV-2001 (first entry)

DE Internalising peptide SEQ ID NO: 21.

XX Internalising peptide; transport; apoptosis; arthritis; cancer;  
KW stem cell; cell differentiation; immune response stimulation;  
KW HIV vaccine.

XX Synthetic.

XX WO200115511-A2.

XX 08-MAR-2001.

XX 31-AUG-2000; 2000WO-US024034.

XX 01-SEP-1999; 99US-0151980P.

XX 13-MAR-2000; 2000US-0188944P.

XX (UYPI-) UNIV PITTSBURGH.

XX Robbins PD, Mi Z, Frizzell R, Glorioso JC, Gambotto A;

XX WPI; 2001-273309/28.

XX Peptides that facilitate uptake and cytoplasmic and/or nuclear transport  
PT of proteins, DNA and viruses, useful, e.g. for facilitating uptake of  
PT antigens in immunogenic compositions.

PS Example 4; Page 117; 129pp; English.

XX The present invention provides the sequences of 75 peptides which  
CC facilitate the uptake and transport of viruses, proteins and nucleic  
CC acids. These internalising peptides can be used for transport into the  
CC cytoplasm or the nucleus. They are useful for facilitating uptake into  
CC the cell, inducing apoptosis, for example in the treatment of arthritis  
CC and cancer, to expand a population of stem cells or differentiated cells,  
CC to stimulate cell differentiation, facilitate the integration of AAV into  
CC the genome of a cell, and to stimulate an immune response, for example in  
CC the case of a HIV vaccine. The present sequence is one of the peptides of  
CC the invention

XX Sequence 11 AA;

Query Match 100.0%; Score 58; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.013;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRKKRRQRRR 11  
| | | | | | | | | |  
DB 1 YGRKKRRQRRR 11

RESULT 15  
AAE05268  
ID AAE05268 standard; peptide; 11 AA.

XX

```

AC AAE05268;
XX
DT 12-SEP-2001 (first entry)
XX
DE Human immunodeficiency virus (HIV) TAT peptide.
XX
KW DNA recombinase domain; protein transduction domain; PTD;
KW gene alteration; TAT; fusion protein; Human immunodeficiency virus; HIV.
XX
OS Human immunodeficiency virus.
XX
PN WO200149832-A2.
XX
PD 12-JUL-2001.
XX
PF 05-JAN-2001; 2001WO-EP0000060.
XX
PR 07-JAN-2000; 2000EP-00100351.
PR 10-NOV-2000; 2000EP-00124595.
XX
PA (ARTE-) ARTEMIS PHARM GMBH.
XX
PI Schwenk F;
XX
DR WPI; 2001-441873/47.
DR N-PSDB; AAD09261.
XX
PT Using site-specific DNA recombinase domain/protein transduction domain
PT fusion proteins for inducing target gene alterations in organisms or cell
PT cultures.
XX
PS Claim 5; Page 70; 85pp; English.
XX
CC The present invention relates to use of fusion proteins comprising a site
CC -specific DNA recombinase domain e.g. Cre and a protein transduction
CC domain (PTD) e.g. the Human immunodeficiency virus (HIV) derived TAT
CC peptide, for preparing an agent for inducing target gene alterations in a
CC living organism or cell culture. The present invention also provides a
CC method for inducing gene alterations in living organisms using the fusion
CC proteins of the invention. The present sequence is HIV TAT peptide
XX
SQ Sequence 11 AA;

Query Match          100.0%; Score 58; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YGRKKRQRR 11
        |||||
Db       1 YGRKKRQRR 11

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Search completed: March 31, 2005, 00:28:21  
Job time : 12.7 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 31, 2005, 00:19:36 ; Search time 129.942 Seconds  
(without alignments)  
918.211 Million cell updates/sec

Title: US-10-049-822A-2  
Perfect score: 1218  
Sequence: 1 MSQSNRELVDLFLSYKLSQK.....FLTGMVAGVLLGLSLFSRK 233

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1218	100.0	233	1 BCLX RAT	P53563 rattus norv
2	1210	99.3	233	1 BCLX MOUSE	Q64373 mus musculu
3	1190	97.7	233	1 BCLX HUMAN	Q07817 homo sapien
4	1190	97.7	233	2 Q76LH7	Q76LH7 canis famil
5	1184	97.2	233	2 Q9N1A2	Q9N1A2 sus scrofa
6	1182	97.0	233	2 Q9MZS7	Q9MZS7 ovis aries
7	1181	96.7	233	2 Q8SQ42	Q8SQ42 felis silve
8	1178	96.4	233	2 Q9MYW4	Q9MYW4 oryctolagus
9	1174	96.4	233	2 Q9MYW4	Q9MYW4 mus musculu
10	1132	92.9	217	2 Q9N3S5	Q9N3S5 rattus norv
11	987	81.0	284	2 Q7TS62	Q7TS62 rattus norv
12	979	80.4	188	2 Q9QW22	Q9QW22 mus musculu
13	979	80.4	235	2 Q35843	Q35843 mus musculu
14	963	79.1	188	2 Q9H1R6	Q9H1R6 homo sapien
15	929	76.3	180	2 Q9BDD5	Q9BDD5 bos taurus
16	917	75.3	229	1 BCLX CHICK	Q07816 gallus gall
17	910	74.7	180	2 Q9BDX7	Q9BDX7 bos taurus
18	901	74.0	219	2 Q99N36	Q99N36 mus musculu
19	824.5	67.7	170	2 Q9WU15	Q9WU15 rattus norv
20	623	51.1	125	2 Q9H1R5	Q9H1R5 homo sapien
21	615.5	50.5	238	2 Q9Q298	Q9Q298 brachydanio
22	529	43.4	201	2 Q6GL15	Q6GL15 xenopus tro
23	516.5	42.4	204	1 AKL1_XENLA	Q91828 xenopus lae
24	515.5	42.3	204	2 Q9QZH2	Q9QZH2 xenopus lae
25	497	40.8	233	1 BCL2 CHICK	Q00709 gallus gall
26	474	38.9	239	2 Q75SV7	Q75SV7 canis famil
27	473.5	38.9	229	1 BCL2 BOVIN	Q02718 bos taurus
28	467.5	38.4	236	1 BCL2_RAT	P49550 rattus norv
29	465.5	38.2	236	1 BCL2_CRILLO	Q91JVB cricetus
30	465.5	38.2	236	2 Q923R6	Q923R6 cricetus
31	464	38.1	239	1 BCL2_HUMAN	P10415 homo sapien

32	462.5	38.0	236	2	Q6R755	Q6R755 canis famil
33	462	37.9	235	2	Q81008	Q81008 felis silve
34	459.5	37.7	236	1	BCL2 MOUSE	P10417 mus musculu
35	458.5	37.6	236	2	Q7TSN8	Q7TSN8 rattus norv
36	458.5	37.6	236	2	Q8BOK4	Q8BOK4 mus musculu
37	439.5	36.1	188	2	Q6GP82	Q6GP82 xenopus lae
38	434.5	35.7	185	2	Q8MJ81	Q8MJ81 bos taurus
39	434	35.6	228	1	AKL1_XENLA	Q91827 xenopus lae
40	433.5	35.6	193	2	Q88996	Q88996 rattus norv
41	433.5	35.6	219	2	Q7TS60	Q7TS60 rattus norv
42	428.5	35.2	192	2	Q6A093	Q6A093 mus musculu
43	428.5	35.2	193	1	BCLW_HUMAN	Q92843 homo sapien
44	428.5	35.2	193	1	BCLW_MOUSE	P70345 mus musculu
45	421	34.6	199	2	Q6NTH7	Q6NTH7 mus musculu

## ALIGNMENTS

RESULT 1  
BCLX RAT  
ID BCLX RAT STANDARD; PRT; 233 AA.  
AC P53563; P70613; P70614; Q62678; Q62836; Q64087; Q64128;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Apoptosis regulator Bcl-X (Bcl-2-like 1 protein).  
GN Name=Bcl2l1; Synonyms=Bclx, B1c2l;  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(S)).  
RC TISSUE=Brain;  
RA Michaelidis T.M.;  
RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RA Wesseling S.L., David G.L., Choi S., Veluona M., Hardwick J.M.;  
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(BETA)).  
RC TISSUE=Thymus;  
RX MEDLINE=96278736; PubMed=8662675; DOI=10.1074/jbc.271.22.13258;  
RA Shiraiwa N., Inohara N., Okada S., Yuzaki M., Shoji S.-I., Ohta S.;  
RT "An additional form of rat Bcl-x, Bcl-xbeta, generated by an unspliced  
RNA, promotes apoptosis in promyeloid cells.";  
J. Biol. Chem. 271:13258-13265 (1996).  
RN [4]  
RP SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(S)).  
RC STRAIN=Sprague-Dawley; TISSUE=Ovary;  
RX MEDLINE=95129487; PubMed=7828536; DOI=10.1210/en.136.1.232;  
RA Tilly J.L., Tilly K.I., Kenton M.L., Johnson A.L.;  
RT "Expression of members of the bcl-2 gene family in the immature rat  
ovary: equine chorionic gonadotropin-mediated inhibition of granulosa  
cell apoptosis is associated with decreased bax and constitutive bcl-2  
and bcl-xlong messenger ribonucleic acid levels.";  
Endocrinology 136:232-241 (1995).  
RN [5]  
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).  
RX MEDLINE=98010630; PubMed=9346936; DOI=10.1074/jbc.272.44.27886;  
RA Arimoto M., Kunishima N., Inohara N., Ishibashi Y., Ohta S.,  
RA Morikawa K.;  
RT "Crystal structure of rat Bcl-xL. Implications for the function of the  
Bcl-2 protein family.";  
J. Biol. Chem. 272:27886-27892 (1997).  
CC -1- FUNCTION: Potent inhibitor of cell death. Isoform Bcl-X(L) anti-  
apoptotic activity is inhibited by association with SIVA isoform  
1. Inhibits activation of caspases (By similarity). Appears to  
regulate cell death by blocking the voltage-dependent anion  
channel (VDAC) by binding to it and preventing the release of the

caspase activator, cytochrome c, from the mitochondrial membrane.  
 The Bcl-X(S) and Bcl-X(beta) isoforms promote apoptosis.  
 -!- SUBUNIT: Bcl-X(L) forms heterodimers with BAX, BAK and Bcl-2 (By similarity). Heterodimerization with BAX does not seem to be required for anti-apoptotic activity (By similarity). Isoform Bcl-X(L) binds to Siva isoform 1 (By similarity).  
 -!- SUBCELLULAR LOCATION: Mitochondrial membranes and perinuclear envelope (By similarity).  
 -!- ALTERNATIVE PRODUCTS:  
 Event-Alternative splicing; Named isoforms=3;  
 Name=Bcl-X(L);  
 IsoId=P53563-1; Sequence=Displayed;  
 Name=Bcl-X(S);  
 IsoId=P53563-2; Sequence=VSP\_000520;  
 Name=Bcl-X(beta);  
 IsoId=P53563-3; Sequence=VSP\_000521;  
 -!- TISSUE SPECIFICITY: Expressed in most tissues. Bcl-X(beta) is specifically expressed in cerebellum, heart, and thymus. In the ovary, the predominant form is Bcl-X(L), with a small but detectable level of Bcl-X(S).  
 -!- DOMAIN: The BH4 domain is required for anti-apoptotic activity. The BH1 and BH2 domains are required for both heterodimerization with other Bcl-2 family members and for repression of cell death.  
 -!- PTM: Proteolytically cleaved by caspases during apoptosis. The cleaved protein, lacking the BH4 domain, has pro-apoptotic activity (By similarity).  
 -!- SIMILARITY: Belongs to the Bcl-2 family.  
 -!- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.  
 -!- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.  
 -!- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.  
 -!- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.  
 -----  
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 EMBL; X82537; CAA57886.1; -;  
 EMBL; X82537; CAA57887.1; -;  
 EMBL; U10579; AAA19257.1; -;  
 EMBL; U72350; AAB17353.1; -;  
 EMBL; U72349; AAB17352.1; -;  
 EMBL; U34963; AAA77686.1; -;  
 EMBL; S76513; AAC60701.2; ALT\_INIT.  
 EMBL; S78284; AAC60702.1; -;  
 PIR; I67431; I67431.  
 PIR; S51761; S51761.  
 PDB; 1AF3; X-ray; @=1-196.  
 RGD; 2200; Bcl2l1.  
 InterPro; IPR000712; Bcl2\_BH.  
 InterPro; IPR003093; Bcl2\_BH4.  
 InterPro; IPR002475; Bcl2\_family.  
 InterPro; IPR004725; Bcl2\_reg.  
 Pfam; PF00452; Bcl-2; 1.  
 Pfam; PF02180; BH4; 1.  
 TIGRFAMs; TIGR00865; bcl-2; 1.  
 PROSITE; PS50062; BCL2\_FAMILY; 1.  
 PROSITE; PS01080; BH1; 1.  
 PROSITE; PS01258; BH2; 1.  
 PROSITE; PS01259; BH3; 1.  
 PROSITE; PS01260; BH4; 1; 1.  
 PROSITE; PS50063; BH4 2; 1.  
 3D-structure; Alternative splicing; Apoptosis; Mitochondrion;  
 Transmembrane. 4 24 BH4.  
 DOMAIN 86 100 BH3.  
 DOMAIN 129 148 BH1.  
 DOMAIN 180 195 BH2.  
 TRANSMEM 210 226 Potential.  
 VARSPPLIC 126 188 Missing (in isoform Bcl-X(S)).

/FTid=VSP\_000520.  
 DTFVDLYGNNAAESRKQGRFNRWFLTGMTVAGVLLGSL  
 PSRK -> VRTTFLVCPPLVCLSSVEIPNCFNPGMVED  
 IDSGDIPGLL (in isoform Bcl-X(beta)).  
 /FTid=VSP\_000521.  
 R -> Q (in Ref. 1).  
 F -> S (in Ref. 2).  
 A -> E (in Ref. 2).  
 I -> L (in Ref. 4).  
 A -> V (in Ref. 4).  
 FF -> SS (in Ref. 4).  
 A -> T (in Ref. 4).  
 A -> P (in Ref. 4).

FT	VARSPPLIC	189	233
FT	CONFLICT	6	6
FT	CONFLICT	12	12
FT	CONFLICT	64	64
FT	CONFLICT	81	81
FT	CONFLICT	119	119
FT	CONFLICT	143	144
FT	CONFLICT	199	199
FT	CONFLICT	201	201
FT	HELIX	4	19
FT	TURN	20	21
FT	TURN	25	28
FT	TURN	82	83
FT	HELIX	84	100
FT	HELIX	106	112
FT	TURN	116	117
FT	HELIX	120	127
FT	HELIX	128	131
FT	TURN	132	133
FT	HELIX	137	156
FT	TURN	157	158
FT	TURN	160	161
FT	HELIX	162	177
FT	TURN	178	178
FT	HELIX	179	184
FT	TURN	185	186
FT	HELIX	187	195
SQ	SEQUENCE	233 AA;	26158 MW; 2B62B6C63864BC8F CRC64;

Query Match 100.0%; Score 1218; DB 1; Length 233;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-97;  
 Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSQNRRLVDFLSYKLSQKGYSWQSDFVEENRTEAPEETEPETPSAINGNPSWHLA 60  
 Db 1 MSQNRRLVDFLSYKLSQKGYSWQSDFVEENRTEAPEETEPETPSAINGNPSWHLA 60

Qy 61 DSPAVNGATGHSSSLDAREVIPMAAVKQALREAGDEPFLRYRRAFSDLTSQLHITPGTAY 120  
 Db 61 DSPAVNGATGHSSSLDAREVIPMAAVKQALREAGDEPFLRYRRAFSDLTSQLHITPGTAY 120

Qy 121 QSPFQVNNELFRDGVNNGRIVAFPSFGALCVESVDKEMQVLVSRIASWMTYLNHLEP 180  
 Db 121 QSPFQVNNELFRDGVNNGRIVAFPSFGALCVESVDKEMQVLVSRIASWMTYLNHLEP 180

Qy 181 WIQENGWDTFVDLYGNNAAESRKQGRFNRWFLTGMTVAGVLLGSLPSRK 233  
 Db 181 WIQENGWDTFVDLYGNNAAESRKQGRFNRWFLTGMTVAGVLLGSLPSRK 233

RESULT 2  
 BCLX\_MOUSE  
 ID\_BCLX\_MOUSE STANDARD; PRT; 233 AA.  
 AC Q64373; Q35844; Q60657; Q61338;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Apoptosis regulator Bcl-X (Bcl-2-like 1 protein).  
 GN Name=Bcl2l1; Synonyms=Bcl121, Bclx;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_taxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM X(L)).  
 RC STRAIN=2A4B;  
 RA Kamesaki H., Michaud G.Y., Takatsu K., Okuma M.;  
 RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.  
 RN [2]



```

Db 121 QSFQVNNELFRDGVNMGRIVAFFSFGALCVESVDKQVLVRSKIASWMTALNDHLEP 180
Qy 181 WIOENGCHDFTVDLYGNNAASRKGQFRNRFWLTGHTVAGVLLGSLFSRK 233
Db 181 WIOENGCHDFTVDLYGNNAASRKGQFRNRFWLTGHTVAGVLLGSLFSRK 233

RESULT 3
BCLX_HUMAN
ID BCLX_HUMAN STANDARD; PRT; 233 AA.
AC Q07817; Q92976;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DE 25-OCT-2004 (Rel. 45, Last annotation update)
DE Apoptosis regulator Bcl-x (Bcl-2-like 1 protein).
GN Name=BCL2L1; Synonyms=BCL2L, BCLX;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(S)).
RX MEDLINE=93364977; PubMed=8358789; DOI=10.1016/0092-8674(93)90508-N;
RA Boise L.H., Gonzalez-Garcia M., Postema C.E., Ding L., Lindsten T.,
RA Turka L.A., Mao X., Nunez G., Thompson C.B.;
RT "bcl-x, a bcl-2-related gene that functions as a dominant regulator of
RT apoptotic cell death."
RL Cell 74:597-608 (1993).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM X(BETA)).
RA Inohara N., Ohta S.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM X(L)).
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Letechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gumaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Hellon E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Greenwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [4]
RP MUTAGENESIS OF G1Y-138, AND HETERO-DIMERIZATION.
RX MEDLINE=95372373; PubMed=7644501;
RA Sedlak T.W., Oltvai Z.N., Yang E., Wang K., Boise L.H., Thompson C.B.,
RA Korsmeyer S.J.;
RT "Multiple Bcl-2 family members demonstrate selective dimerizations
RT with Bax."
RL Proc. Natl. Acad. Sci. U.S.A. 92:7834-7838 (1995).
RN [5]
RP MUTAGENESIS OF BH1 AND BH2 DOMAINS.
RX MEDLINE=96170038; PubMed=8596636; DOI=10.1038/379554a0;
RA Cheng E.H.-Y., Levine B., Boise L.H., Thompson C.B., Hardwick J.M.,
RA Korsmeyer S.J.;
RT "Bax-independent inhibition of apoptosis by Bcl-XL."
RL Nature 379:554-556 (1996).
RN [6]
RP INTERACTION WITH SIVA.

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RX MEDLINE=22008092; PubMed=12011449; DOI=10.1073/pnas.102182299;
RA Xue L., Chu P., Cheng Y., Sun X., Borthakur A., Ramarao M., Pandey P.,
RA Wu M., Schlossman S.F., Prasad K.V.S.;
RT "Siva-1 binds to and inhibits Bcl-X(L)-mediated protection against UV
RT radiation-induced apoptosis."
RL Proc. Natl. Acad. Sci. U.S.A. 99:6925-6930 (2002).
RN [7]
RP STRUCTURE BY NMR OF 1-209.
RX MEDLINE=97172562; PubMed=9020082; DOI=10.1126/science.275.5302.983;
RA Sattler M., Liang H., Nettlesheim D., Meadows R.P., Harlan J.E.,
RA Eberstadt M., Yoon H.S., Shuker S.B., Chang B.S., Minn A.J.,
RA Thompson C.B., Fesik S.W.;
RT "Structure of Bcl-XL-Bak peptide complex: recognition between
RT regulators of apoptosis."
RL Science 275:983-986 (1997).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS), AND STRUCTURE BY NMR OF 1-209.
RX MEDLINE=96256675; PubMed=8692274; DOI=10.1038/381335a0;
RA Muchmore S.W., Sattler M., Liang H., Meadows R.P., Harlan J.E.,
RA Yoon H.S., Nettlesheim D., Chang B.S., Thompson C.B., Wong S.L.,
RA Ng S.L., Fesik S.W.;
RT "X-ray and NMR structure of human Bcl-XL, an inhibitor of programmed
RT cell death."
RL Nature 381:335-341 (1996).
RN [9]
RP CLEAVAGE BY CASPASES, AND MUTAGENESIS OF ASP-61.
RX MEDLINE=98118550; PubMed=9435230; DOI=10.1073/pnas.95.2.554;
RA Clem R.J., Cheng E.H.-Y., Karp C.L., Kirsch D.G., Ueno K.,
RA Takahashi A., Kastan M.B., Griffin D.E., Earnshaw W.C., Veliuona M.A.,
RA Hardwick J.M.;
RT "Modulation of cell death by Bcl-XL through caspase interaction."
RL Proc. Natl. Acad. Sci. U.S.A. 95:554-559 (1998).
CC -1- FUNCTION: Potent inhibitor of cell death. Isoform Bcl-X(L) anti-
CC apoptotic activity is inhibited by association with SIVA isoform
CC 1. Inhibits activation of caspases (By similarity). Appears to
CC regulate cell death by blocking the voltage-dependent anion
CC channel (VDAC) by binding to it and preventing the release of the
CC caspase activator, cytochrome c, from the mitochondrial membrane.
CC The Bcl-X(S) isoform promotes apoptosis.
CC -1- SUBUNIT: Bcl-X(L) forms heterodimers with BAX, BAK and Bcl-2.
CC Heterodimerization with BAX does not seem to be required for anti-
CC apoptotic activity. Isoform Bcl-X(L) binds to Siva isoform 1.
CC -1- SUBCELLULAR LOCATION: Mitochondrial membranes and perinuclear
CC envelope (By similarity).
CC -1- ALTERNATIVE PRODUCTS:
CC Name=Bcl-X(L);
CC IsoId=Q07817-1; Sequence=VSP_000515;
CC Name=Bcl-X(S);
CC IsoId=Q07817-2; Sequence=VSP_000516;
CC Name=Bcl-X(beta);
CC IsoId=Q07817-3; Sequence=VSP_000516;
CC -1- TISSUE SPECIFICITY: Bcl-X(S) is expressed at high levels in cells
CC that undergo a high rate of turnover, such as developing
CC lymphocytes. In contrast, Bcl-X(L) is found in tissues containing
CC long-lived postmitotic cells, such as adult brain.
CC -1- DOMAIN: The BH4 domain is required for anti-apoptotic activity.
CC The BH1 and BH2 domains are required for both heterodimerization
CC with other Bcl-2 family members and for repression of cell death.
CC -1- PTM: Proteolytically cleaved by caspases during apoptosis. The
CC cleaved protein, lacking the BH4 domain, has pro-apoptotic
CC activity.
CC -1- SIMILARITY: Belongs to the Bcl-2 family.
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC

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ID Q9N1A2 PRELIMINARY; PRT; 233 AA.  
 AC Q9N1A2;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Anti-apoptotic regulator Bcl-xL.  
 GN Name=bcl-xL;  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 OX NCBI\_TaxID=9823;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Heart;  
 RA Lee T.L., Canty J.M.;  
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF216205; AAF3212.1; -.  
 DR HSSP; Q07817; IR2D.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR InterPro; IPR000712; Bcl2\_BH.  
 DR InterPro; IPR003093; Bcl2\_BH4.  
 DR InterPro; IPR002475; Bcl2\_family.  
 DR InterPro; IPR004725; Bcl2\_reg.  
 DR Pfam; PF00452; Bcl-2; 1.  
 DR Pfam; PF02180; BH4; 1.  
 DR SMART; SM00337; BCL; 1.  
 DR SMART; SM00265; BH4; 1.  
 DR TIGRFAMs; TIGR00865; bcl-2; 1.  
 DR PROSITE; PS0062; BCL2\_FAMILY; 1.  
 DR PROSITE; PS01080; BH1; 1.  
 DR PROSITE; PS01258; BH2; 1.  
 DR PROSITE; PS01259; BH3; 1.  
 DR PROSITE; PS01260; BH4; 1.  
 DR PROSITE; PS0063; BH4\_2; 1.  
 DR PROSITE; PS0063; BH4\_2; 1.  
 SQ SEQUENCE 233 AA; 26047 MW; 2FA312818B25E17D CRC64;  
  
 Query Match 97.2%; Score 1184; DB 2; Length 233;  
 Best Local Similarity 97.0%; Pred. No. 3.9e-94;  
 Matches 226; Conservative 4; Mismatches 4; Indels 0; Gaps 0;  
  
 QY 1 MSQSNRELVDVFLSYKLSQKGYSWQSFSDVEENRTEAPEETEPEETPSAINGNPSWHLA 60  
 DB 1 MSQSNRELVDVFLSYKLSQKGYSWQSFSDVEENRTEAPEETEPEETPSAINGNPSWHLA 60  
  
 QY 61 DSPAVNGATGSHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAPSDLTSLQHTTPGTAY 120  
 DB 61 DSPAVNGATGSHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAPSDLTSLQHTTPGTAY 120  
  
 QY 121 QSFQVNVNLFPRDGVNMGRIVAFPSFGGALCVESVDKEMQVLVSRISWMTATYLNHLEP 180  
 DB 121 QSFQVNVNLFPRDGVNMGRIVAFPSFGGALCVESVDKEMQVLVSRISWMTATYLNHLEP 180  
  
 QY 181 WIQENGWDFTVDLYGNNAAESRKGQERFNRWFLTGMTVAGVVLGSLFSRK 233  
 DB 181 WIQENGWDFTVDLYGNNAAESRKGQERFNRWFLTGMTVAGVVLGSLFSRK 233  
  
 RESULT 6  
 ID Q9M2S7 PRELIMINARY; PRT; 233 AA.  
 AC Q9M2S7;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DE Bcl-x long protein.  
 OS Ovis aries (Sheep).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Caprinae; Ovis.  
 OX NCBI\_TaxID=9940;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC TISSUE=Ovary;  
 RA Murray J.P., Dong Y.B., Leigh A.J., Scaramuzzi R.J., Carter N.D.;  
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF164517; AAF89532.1; -.  
 DR HSSP; P53563; IAP3.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR InterPro; IPR000712; Bcl2\_BH.  
 DR InterPro; IPR003093; Bcl2\_BH4.  
 DR InterPro; IPR002475; Bcl2\_family.  
 DR InterPro; IPR004725; Bcl2\_reg.  
 DR Pfam; PF00452; Bcl-2; 1.  
 DR Pfam; PF02180; BH4; 1.  
 DR SMART; SM00337; BCL; 1.  
 DR SMART; SM00265; BH4; 1.  
 DR TIGRFAMs; TIGR00865; bcl-2; 1.  
 DR PROSITE; PS0062; BCL2\_FAMILY; 1.  
 DR PROSITE; PS01080; BH1; 1.  
 DR PROSITE; PS01258; BH2; 1.  
 DR PROSITE; PS01259; BH3; 1.  
 DR PROSITE; PS01260; BH4; 1.  
 DR PROSITE; PS0063; BH4\_2; 1.  
 DR PROSITE; PS0063; BH4\_2; 1.  
 SQ SEQUENCE 233 AA; 26134 MW; 012BFA1382762915 CRC64;  
  
 Query Match 97.0%; Score 1182; DB 2; Length 233;  
 Best Local Similarity 97.0%; Pred. No. 5.8e-94;  
 Matches 226; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
  
 QY 1 MSQSNRELVDVFLSYKLSQKGYSWQSFSDVEENRTEAPEETEPEETPSAINGNPSWHLA 60  
 DB 1 MSQSNRELVDVFLSYKLSQKGYSWQSFSDVEENRTEAPEETEPEETPSAINGNPSWHLA 60  
  
 QY 61 DSPAVNGATGSHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAPSDLTSLQHTTPGTAY 120  
 DB 61 DSPAVNGATGSHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAPSDLTSLQHTTPGTAY 120  
  
 QY 121 QSFQVNVNLFPRDGVNMGRIVAFPSFGGALCVESVDKEMQVLVSRISWMTATYLNHLEP 180  
 DB 121 QSFQVNVNLFPRDGVNMGRIVAFPSFGGALCVESVDKEMQVLVSRISWMTATYLNHLEP 180  
  
 QY 181 WIQENGWDFTVDLYGNNAAESRKGQERFNRWFLTGMTVAGVVLGSLFSRK 233  
 DB 181 WIQENGWDFTVDLYGNNAAESRKGQERFNRWFLTGMTVAGVVLGSLFSRK 233  
  
 RESULT 7  
 ID BCLX\_PIG STANDARD; PRT; 233 AA.  
 AC O77737;  
 DT 15-JUL-1999 (Rel. 38, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Apoptosis regulator Bcl-X (Bcl-2-like 1 protein).  
 GN Name=BCL2L1; Synonyms=BCLX, BLC2L;  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 OX NCBI\_TaxID=9823;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99171363; PubMed=10072723; DOI=10.1006/jmcc.1998.0855;  
 RA Bartling B., Hoffmann J., Holtz J., Schulz R., Heusch G., Damer D.;  
 RT "Quantification of cardioprotective gene expression in porcine short-term hibernating myocardium."  
 RL J. Mol. Cell. Cardiol. 31:147-158(1999).  
 CC -1- FUNCTION: Potent inhibitor of cell death. Isoform Bcl-X(L) anti-apoptotic activity is inhibited by association with SIVA isoform 1. Inhibits activation of caspases (By similarity). Appears to regulate cell death by blocking the voltage-dependent anion channel (VDAC) by binding to it and preventing the release of the caspase activator, cytochrome c, from the mitochondrial membrane.  
 CC -1- SUBUNIT: Bcl-X(L) forms heterodimers with BAX, BAK and Bcl-2 (By similarity). Heterodimerization with BAX does not seem to be

required for anti-apoptotic activity (By similarity). Isoform Bcl-X(L) binds to Siva isoform 1 (By similarity).

-!- SUBCELLULAR LOCATION: Mitochondrial membranes and perinuclear envelope (By similarity).

-!- DOMAIN: The BH4 domain is required for anti-apoptotic activity. The BH1 and BH2 domains are required for both heterodimerization with other Bcl-2 family members and for repression of cell death.

-!- PTM: Proteolytically cleaved by caspases during apoptosis (By similarity). The cleaved protein, lacking the BH4 domain, has pro-apoptotic activity (By similarity).

-!- SIMILARITY: Belongs to the Bcl-2 family.

-!- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.

-!- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.

-!- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.

-!- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.

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EMBL; AJ001203; CAA04597.1; -  
 HSP; Q07817; IMAZ.  
 InterPro; IPR000712; Bcl2\_BH.  
 InterPro; IPR003093; Bcl2\_BH4.  
 InterPro; IPR002475; BCL2\_family.  
 InterPro; IPR004725; BCL2\_reg.  
 Pfam; PF00452; Bcl-2; 1.  
 Pfam; PF02180; BH4; 1.  
 TIGRFAMs; TIGR00865; bcl-2; 1.  
 PROSITE; PS00062; BCL2\_FAMILY; 1.  
 PROSITE; PS01080; BH1; 1.  
 PROSITE; PS01258; BH2; 1.  
 PROSITE; PS01259; BH3; 1.  
 PROSITE; PS01259; BH3; 1.  
 PROSITE; PS01260; BH4; 1; 1.  
 PROSITE; PS00063; BH4\_2; 1.  
 Apoptosis; Mitochondrion; Transmembrane.  
 DOMAIN 4 24 BH4.  
 DOMAIN 86 100 BH3.  
 DOMAIN 129 148 BH1.  
 DOMAIN 180 195 BH2.  
 TRANSMEM 210 226 Potential.  
 SEQUENCE 233 AA; 26061 MW; 18BF6FA0441912B2 CRC64;

Query Match 97.0%; Score 1181; DB 1; Length 233;  
 Best Local Similarity 96.6%; Pred. No. 7e-94;  
 Matches 225; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MSQSNRELVDVFLSYKLSQKGSWSQSDVENRTEAPEETPERETPSAINGNPSWHLA 60  
 Db 1 MSQSNRELVDVFLSYKLSQKGSWSQSDVENRTEAPEETPERETPSAINGNPSWHLA 60  
 Qy 61 DSPAVNGATGHSSSLDAREVTPMAAVKQALREAGDEFEFLRYRAFSDLTSLQHIPTGTAY 120  
 Db 61 DSPAVNGATGHSSSLDAREVTPMAAVKQALREAGDEFEFLRYRAFSDLTSLQHIPTGTAY 120  
 Qy 121 QSFQVNVNELFRDGVNWRGRIVAFFSFGGALCVESVDKEMQVLVSRIASWMTATYLNHLEP 180  
 Db 121 QSFQVNVNELFRDGVNWRGRIVAFFSFGGALCVESVDKEMQVLVSRIASWMTATYLNHLEP 180  
 Qy 181 WIQENGWDVTFVLYGNNAASERKQGRFNRWFLTGMTVAGVLLGSLFSRK 233  
 Db 181 WIQENGWDVTFVLYGNNAASERKQGRFNRWFLTGMTVAGVLLGSLFSRK 233

## RESULT 8

Q8SQ42 ID Q8SQ42 PRELIMINARY; PRT; 233 AA.  
 AC Q8SQ42;  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)

DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update).  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Bcl-x1 protein.  
 GN Name=bcl-x1;  
 OS Felis silvestris catus (Cat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
 OX NCBI\_TaxID=9685;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Nagafuchi S., Sano J., Kano R., Hasegawa A.;  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB080951; BAB85856.2; -  
 DR HSP; Q07817; IMAZ.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0042981; P:regulation of apoptosis; IEA.  
 DR InterPro; IPR000712; Bcl2\_BH.  
 DR InterPro; IPR003093; Bcl2\_BH4.  
 DR InterPro; IPR002475; BCL2\_family.  
 DR InterPro; IPR004725; BCL2\_reg.  
 Pfam; PF00452; Bcl-2; 1.  
 Pfam; PF02180; BH4; 1.  
 SMART; SM00337; BCL; 1.  
 SMART; SM00265; BH4; 1.  
 TIGRFAMs; TIGR00865; bcl-2; 1; 1.  
 PROSITE; PS00062; BCL2\_FAMILY; 1.  
 PROSITE; PS01080; BH1; 1.  
 PROSITE; PS01258; BH2; 1.  
 PROSITE; PS01259; BH3; 1.  
 PROSITE; PS01260; BH4; 1; 1.  
 PROSITE; PS00063; BH4\_2; 1.  
 SEQUENCE 233 AA; 26017 MW; CD17F24FE9D47BC9 CRC64;

Query Match 96.7%; Score 1178; DB 2; Length 233;  
 Best Local Similarity 97.0%; Pred. No. 1.3e-93;  
 Matches 226; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MSQSNRELVDVFLSYKLSQKGSWSQSDVENRTEAPEETPERETPSAINGNPSWHLA 60  
 Db 1 MSQSNRELVDVFLSYKLSQKGSWSQSDVENRTEAPEETPERETPSAINGNPSWHLA 60  
 Qy 61 DSPAVNGATGHSSSLDAREVTPMAAVKQALREAGDEFEFLRYRAFSDLTSLQHIPTGTAY 120  
 Db 61 DSPAVNGATGHSSSLDAREVTPMAAVKQALREAGDEFEFLRYRAFSDLTSLQHIPTGTAY 120  
 Qy 121 QSFQVNVNELFRDGVNWRGRIVAFFSFGGALCVESVDKEMQVLVSRIASWMTATYLNHLEP 180  
 Db 121 QSFQVNVNELFRDGVNWRGRIVAFFSFGGALCVESVDKEMQVLVSRIASWMTATYLNHLEP 180  
 Qy 181 WIQENGWDVTFVLYGNNAASERKQGRFNRWFLTGMTVAGVLLGSLFSRK 233  
 Db 181 WIQENGWDVTFVLYGNNAASERKQGRFNRWFLTGMTVAGVLLGSLFSRK 233

## RESULT 9

Q9MYW4 ID Q9MYW4 PRELIMINARY; PRT; 233 AA.  
 AC Q9MYW4;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Bcl-X.  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RA Knott J.C., Robertson L., James E.R.;  
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY005131; AAF88137.1; -  
 DR HSP; P53563; IAF3.  
 DR GO; GO:0016020; C:membrane; IEA.



DR GO; GO:0042981; P:regulation of apoptosis; IEA.  
 DR InterPro; IPR000712; Bcl2\_BH.  
 DR InterPro; IPR003093; Bcl2\_BH4.  
 DR InterPro; IPR002475; Bcl2\_family.  
 DR InterPro; IPR004725; Bcl2\_reg.  
 DR Pfam; PF00452; Bcl-2; 1.  
 DR Pfam; PF02180; BH4; 1.  
 DR SMART; SM00337; BCL; 1.  
 DR SMART; SM00265; BH4; 1.  
 DR TIGRFAMs; TIGR00865; bcl-2; 1.  
 DR PROSITE; PS50062; BCL2\_FAMILY; 1.  
 DR PROSITE; PS01080; BH1; 1.  
 DR PROSITE; PS01258; BH2; 1.  
 DR PROSITE; PS01259; BH3; 1.  
 DR PROSITE; PS01260; BH4; 1.  
 DR PROSITE; PS50063; BH4\_2; 1.  
 SQ SEQUENCE 233 AA; 25986 MW; 12F0F30344D53F93 CRC64;

Query Match 96.4%; Score 1174; DB 2; Length 233;  
 Best Local Similarity 96.1%; Pred. No. 2.8e-93;  
 Matches 224; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MSQSNRELVDVFLSYKLSQKGYSWQSDVEENRTEAPEETEPEETPSAINGNPSWHLA 60  
 Db 1 MSQSNRELVDVFLSYKLSQKGYSWQSDVEENRTEAPEETEPEETPSAINGNPSWHLA 60

Qy 61 DSPAVNGATGHSSSLDAREVPMRAVKQALREAGDEPELRVRRAFSDLTSLQHTTPGTAY 120  
 Db 61 DSPAVNGATGHSSSLDAREVPMRAVKQALREAGDEPELRVRRAFSDLTSLQHTTPGTAY 120

Qy 121 QSFEQVNVNLFPRDGVNWRGRIVAFFSFGGALCVESVDKEMQVLVSRIASWMTYLNHLEP 180  
 Db 121 QSFEQVNVNLFPRDGVNWRGRIVAFFSFGGALCVESVDKEMQVLVSRIASWMTYLNHLEP 180

Qy 181 WIQENGWDTFTVDLYGNNAAESRKQGRFNRFMTGTVAGVLLGSLFSRK 233  
 Db 181 WIQENGWDTFTVDLYGNNAAESRKQGRFNRFMTGTVAGVLLGSLFSRK 233

RESULT 10  
 Q99N35 PRELIMINARY; PRT; 217 AA.  
 AC Q99N35; STRAIN=Sprague-Dawley;  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE B-cell leukemia/lymphoma x (Fragment).  
 GN Name=Bclx;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129/SVJ;  
 RX MEDLINE=22202614; PubMed=1231327; DOI=10.1016/S0161-5890(02)00049-4;  
 RA Yang X.-F., Ye Q., Press B., Han R.-Z., Bassing C.H., Sleckman B.P.,  
 RA Alt F.W., Cantor H.;  
 RT "Analysis of the complex genomic structure of Bcl-x and its  
 RT relationship to Bcl-xgamma expression after CD28-dependent  
 RT costimulation."  
 RL Mol. Immunol. 39:45-55(2002).  
 DR EMBL; AF133282; AAK15455.1; -.  
 DR EMBL; AF133281; AAK15455.1; JOINED.  
 DR HSSP; P53563; IAF3.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0042981; P:regulation of apoptosis; IEA.  
 DR InterPro; IPR000712; Bcl2\_BH.  
 DR InterPro; IPR002475; Bcl2\_family.  
 DR InterPro; IPR004725; Bcl2\_reg.  
 DR Pfam; PF00452; Bcl-2; 1.  
 DR SMART; SM00337; BCL; 1.  
 DR TIGRFAMs; TIGR00865; bcl-2; 1.

DR PROSITE; PS50062; BCL2\_FAMILY; 1.  
 DR PROSITE; PS01080; BH1; 1.  
 DR PROSITE; PS01258; BH2; 1.  
 DR PROSITE; PS01259; BH3; 1.  
 FT NON\_TER 1  
 SQ SEQUENCE 217 AA; 24234 MW; 3B5A4E809A7DEF18 CRC64;

Query Match 92.9%; Score 1132; DB 2; Length 217;  
 Best Local Similarity 99.5%; Pred. No. 1.1e-89;  
 Matches 216; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 17 LSQKGYSWQSDVEENRTEAPEETEPEETPSAINGNPSWHLADSPAVNGATGHSSSLD 76  
 Db 1 LSQKGYSWQSDVEENRTEAPEETEPEETPSAINGNPSWHLADSPAVNGATGHSSSLD 60

Qy 77 AREVPMRAVKQALREAGDEPELRVRRAFSDLTSLQHTTPGTAYQSFEQVNVNLFPRDGVN 136  
 Db 61 AREVPMRAVKQALREAGDEPELRVRRAFSDLTSLQHTTPGTAYQSFEQVNVNLFPRDGVN 120

Qy 137 WGRIVAFSFGGALCVESVDKEMQVLVSRIASWMTYLNHLEPWIQENGWDTFTVDLYG 196  
 Db 121 WGRIVAFSFGGALCVESVDKEMQVLVSRIASWMTYLNHLEPWIQENGWDTFTVDLYG 180

Qy 197 NNAAESRKQGRFNRFMTGTVAGVLLGSLFSRK 233  
 Db 181 NNAAESRKQGRFNRFMTGTVAGVLLGSLFSRK 217

RESULT 11  
 Q7TS62 PRELIMINARY; PRT; 284 AA.  
 AC Q7TS62; STRAIN=Sprague-Dawley;  
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Bcl-xbeta.  
 GN Name=Bcl-x;  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Sprague-Dawley;  
 RX MEDLINE=22672518; PubMed=12787069;  
 RA Itoh T., Itoh A., Pleasure D.;  
 RT "Bcl-2-related protein family gene expression during oligodendroglial  
 RT differentiation."  
 RL J. Neurochem. 85:1500-1512(2003).  
 DR EMBL; AY141038; AANI7784.1; -.  
 DR HSSP; P53563; IAF3.  
 DR GO; GO:0042981; P:regulation of apoptosis; IEA.  
 DR InterPro; IPR000712; Bcl2\_BH.  
 DR InterPro; IPR003093; Bcl2\_BH4.  
 DR Pfam; PF00452; Bcl-2; 1.  
 DR Pfam; PF02180; BH4; 1.  
 DR SMART; SM00337; BCL; 1.  
 DR SMART; SM00265; BH4; 1.  
 DR PROSITE; PS50062; BCL2\_FAMILY; 1.  
 DR PROSITE; PS01080; BH1; 1.  
 DR PROSITE; PS01259; BH3; 1.  
 DR PROSITE; PS01260; BH4; 1.  
 DR PROSITE; PS50063; BH4\_2; 1.  
 SQ SEQUENCE 284 AA; 31776 MW; B8F35F641D4E029E CRC64;

Query Match 81.0%; Score 987; DB 2; Length 284;  
 Best Local Similarity 100.0%; Pred. No. 5.3e-77;  
 Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSQSNRELVDVFLSYKLSQKGYSWQSDVEENRTEAPEETEPEETPSAINGNPSWHLA 60  
 Db 1 MSQSNRELVDVFLSYKLSQKGYSWQSDVEENRTEAPEETEPEETPSAINGNPSWHLA 60



Qy 61 DSPAVNGATGSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHTTPGTAY 120  
 |||||  
 Db 61 DSPAVNGATGSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHTTPGTAY 120  
 |||||  
 Qy 121 QSFQVNVNELFRDGVNNGRIVAFPSFGALCVESVDKEMQVLVSRIASWMTATYLNHLEP 180  
 |||||  
 Db 121 QSFQVNVNELFRDGVNNGRIVAFPSFGALCVESVDKEMQVLVSRIASWMTATYLNHLEP 180  
 |||||  
 Qy 181 WIQENGW 188  
 |||||  
 Db 181 WIQENGW 188  
 |||||

RESULT 12

Q9QWX2 PRELIMINARY; PRT; 188 AA.

AC Q9QWX2; 01-MAY-2000 (Tremblrel. 13, Created)

DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)

DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)

DE Bcl-x (Fragment).

GN Name=Bcl2l1; Synonyms=Bcl2l1;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20350651; PubMed=10894153; DOI=10.1210/me.14.7.1038;

RA Rucker E.B. III, Dierisseau P., Wagner K.U., Garrett L.,

RA Wynshaw-Boris A., Flaws J.A., Hennighausen L.;

RT "Bcl-x and Bax regulate mouse primordial germ cell survival and

RT apoptosis during embryogenesis.";

RL Mol. Endocrinol. 14:1038-1052(2000).

RN [2]

RP SEQUENCE FROM N.A.

RA Rucker E. III, Dierisseau P., Herring S., Wagner K.-U.,

RA Hennighausen L.;

RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF088904; AAC7232.1; --

DR HSSP; P53563; 1AF3.

DR MGD; MGI:88139; Bcl2l1.

DR GO; GO:0005739; C:mitochondrion; IDA.

DR GO; GO:0005515; F:protein binding; IPI.

DR GO; GO:0006916; P:anti-apoptosis; IDA.

DR GO; GO:0006915; P:apoptosis; IDA.

DR GO; GO:0009314; P:response to radiation; IMP.

DR InterPro; IPR000712; Bcl2 BH.

DR InterPro; IPR003093; Bcl2\_FAMILY.

DR Pfam; PF00452; Bcl-2; 1.

DR SMART; SM00337; BCL; 1.

DR SMART; SM00265; BH4; 1.

DR PROSITE; PS00062; BCL2\_FAMILY; 1.

DR PROSITE; PS01080; BH1; 1.

DR PROSITE; PS01259; BH3; 1.

DR PROSITE; PS01260; BH4; 1.

DR PROSITE; PS00063; BH4\_2; 1.

FT NON TER 188

SQ SEQUENCE 188 AA; 21126 MW; 4562F8356D248E52 CRC64;

Query Match 80.4%; Score 979; DB 2; Length 188;

Best Local Similarity 99.5%; Pred. No. 1.5e-76;

Matches 187; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSQSNRELVDVFLSYKLSQKGYSWQSFSDVEENRTEAPEETEPEPTPSAINGNPSWHLA 60  
 |||||  
 Db 1 MSQSNRELVDVFLSYKLSQKGYSWQSFSDVEENRTEAPEETEPEPTPSAINGNPSWHLA 60  
 |||||

Qy 61 DSPAVNGATGSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHTTPGTAY 120  
 |||||

Db 61 DSPAVNGATGSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHTTPGTAY 120  
 |||||  
 Qy 121 QSFQVNVNELFRDGVNNGRIVAFPSFGALCVESVDKEMQVLVSRIASWMTATYLNHLEP 180  
 |||||  
 Db 121 QSFQVNVNELFRDGVNNGRIVAFPSFGALCVESVDKEMQVLVSRIASWMTATYLNHLEP 180  
 |||||  
 Qy 181 WIQENGW 188  
 |||||  
 Db 181 WIQENGW 188  
 |||||

RESULT 13

O35843 PRELIMINARY; PRT; 235 AA.

AC O35843; 01-JAN-1998 (Tremblrel. 05, Created)

DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)

DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)

DE Bcl-x-gamma.

GN Name=Bcl2l1; Synonyms=Bcl2l1;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX STRAIN=B6/CBA; TISSUE=Thymus;

RX MEDLINE=98051053; PubMed=9390687; DOI=10.1016/S1074-7613(00)80384-2;

RA Yang X.-F., Weber G.F., Cantor H.;

RT "A novel Bcl-x isoform connected to the T cell receptor regulates

RT apoptosis in T cells.";

RL Immunity 7:629-639(1997).

DR EMBL; U51277; AAC53458.1; --

DR HSSP; P53563; 1AF3.

DR MGD; MGI:88139; Bcl2l1.

DR GO; GO:0005739; C:mitochondrion; IDA.

DR GO; GO:0005515; F:protein binding; IPI.

DR GO; GO:0006916; P:anti-apoptosis; IDA.

DR GO; GO:0006915; P:apoptosis; IDA.

DR GO; GO:0009314; P:response to radiation; IMP.

DR InterPro; IPR000712; Bcl2 BH.

DR InterPro; IPR003093; Bcl2\_FAMILY.

DR InterPro; IPR002475; Bcl2\_reg.

DR Pfam; PF00452; Bcl-2; 1.

DR Pfam; PF02180; BH4; 1.

DR SMART; SM00337; BCL; 1.

DR SMART; SM00265; BH4; 1.

DR TIGRFAMs; TIGR00865; bcl-2; 1.

DR PROSITE; PS00062; BCL2\_FAMILY; 1.

DR PROSITE; PS01080; BH1; 1.

DR PROSITE; PS01259; BH3; 1.

DR PROSITE; PS01260; BH4; 1.

DR PROSITE; PS00063; BH4\_2; 1.

SQ SEQUENCE 235 AA; 26122 MW; 649D914C2D5378F6 CRC64;

Query Match 80.4%; Score 979; DB 2; Length 235;

Best Local Similarity 99.5%; Pred. No. 2e-76;

Matches 187; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSQSNRELVDVFLSYKLSQKGYSWQSFSDVEENRTEAPEETEPEPTPSAINGNPSWHLA 60  
 |||||  
 Db 1 MSQSNRELVDVFLSYKLSQKGYSWQSFSDVEENRTEAPEETEPEPTPSAINGNPSWHLA 60  
 |||||

Qy 61 DSPAVNGATGSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHTTPGTAY 120  
 |||||

Db 61 DSPAVNGATGSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHTTPGTAY 120  
 |||||

Qy 121 QSFQVNVNELFRDGVNNGRIVAFPSFGALCVESVDKEMQVLVSRIASWMTATYLNHLEP 180  
 |||||

Db 121 QSFQVNVNELFRDGVNNGRIVAFPSFGALCVESVDKEMQVLVSRIASWMTATYLNHLEP 180  
 |||||

Qy 181 WIQENGW 188  
 |||||

RESULT 15	Q9BDD5	Q9BDD5	PRELIMINARY;	PRT;	180 AA.
ID	Q9BDD5	Q9BDD5			
AC	Q9BDD5	Q9BDD5			
DT	01-JUN-2001	(TrEMBLrel. 17, Created)			
DT	01-JUN-2001	(TrEMBLrel. 17, Last sequence update)			
DT	05-JUL-2004	(TrEMBLrel. 27, Last annotation update)			
DE	Anti-apoptotic regulator Bcl-xL (Fragment).				
OS	Bos taurus (Bovine).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;				
OC	Bovinae; Bos.				
OX	NCBI_TaxID=9913;				

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 31, 2005, 00:22:11 ; Search time 30.4692 Seconds  
(without alignments)  
735.775 Million cell updates/sec

Title: US-10-049-822A-2  
Perfect score: 1218  
Sequence: 1 MSQSNRELVDVFLSYKLSQK.....FLGTMVAGVLLGSLFSRK 233

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1214	99.7	233	2 S51761	BCL-X protein - ra
2	1210	99.3	233	2 I49056	bcl-x long - mouse
3	1187	97.5	233	2 I67431	BCL-X-Long - rat
4	1184	97.2	233	2 B47537	apoptosis regulato
5	1006	82.6	214	2 I49057	bcl-x transmembran
6	963	79.1	227	2 JB0203	apoptosis regulato
7	825.5	67.8	170	2 I49055	bcl-x short - mous
8	818.5	67.2	176	2 I67435	gene bcl-xshort pr
9	732	60.1	190	2 A47537	apoptosis regulato
10	497	40.8	233	2 A37332	transforming prote
11	474.5	39.0	232	2 S24390	transforming prote
12	465.5	38.2	236	2 JG7383	B-cell lymphoma 2
13	465	38.2	236	2 I67432	BCL-2 - rat (fragm
14	464	38.1	239	1 TVH011	transforming prote
15	460.5	37.8	236	2 I53744	gene bcl-2 protein
16	457	37.5	236	1 TVWSA1	transforming prote
17	447.5	36.7	216	2 B37332	transforming prote
18	423.5	34.8	205	1 TVH0B1	transforming prote
19	422	34.6	199	1 TVWSB1	transforming prote
20	315	25.9	154	2 I58194	gene bcl-2 protein
21	182	14.9	211	2 S58875	cdn-2 protein - hu
22	181	14.9	211	2 S58873	Bak protein - huma
23	167	13.7	177	2 S54778	NR-13 protein - qu
24	166	13.6	192	2 D47538	bcl-2-associated p
25	166	13.6	192	2 A47538	bcl-2-associated p
26	165.5	13.6	133	2 I53295	bcl-2-associated p
27	152	12.5	143	2 I38921	bcl-2-associated p
28	150.5	12.4	179	2 JC7255	Bax-delta protein
29	148.5	12.2	218	2 B47538	bcl-2-associated p

30	148	12.2	255	2 JC7567	Mcl-1a protein - 2
31	144	11.8	172	2 I49449	hemopoietic-specif
32	137.5	11.3	350	2 A47476	BCL2 homolog MCL1
33	135	11.1	261	2 H88578	protein ced-9 (imp
34	135	11.1	280	2 A53189	apoptosis suppress
35	130	10.7	175	2 I39055	Bcl-2 related - hu
36	102	8.4	160	2 G36807	hypothetical prote
37	94.5	7.8	191	1 Q0B84	BHRF1 protein - hu
38	93	7.6	780	2 T09485	cold-induced prote
39	91	7.5	801	2 B83195	hypothetical prote
40	91	7.5	1215	2 E84480	probable retroelem
41	89.5	7.3	462	2 E82683	RNA polymerase sig
42	87	7.1	442	2 T39883	zucotin-like protei
43	86.5	7.1	1061	1 DJAD12	DNA-directed DNA p
44	86	7.1	544	2 S19149	thioglucoisidase (E
45	86	7.1	658	2 S37494	squalene-hopene cy

ALIGNMENTS

RESULT 1

S51761  
BCL-X protein - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 07-May-1995 #sequence\_revision 01-Sep-1995 #text\_change 09-Jul-2004  
C;Accession: S51761; S51762  
R;Michaelidis, T.M.  
submitted to the EMBL Data Library, November 1994  
A;Reference number: S51761  
A;Accession: S51761  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-233 <MIC>  
A;Cross-references: UNIPROT:P53563; EMBL:X82537; NID:g607176; PIDN:CAA57886.1; PID:g6071  
A;Experimental source: embryonic; brain  
A;Accession: S51762  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-125,189-233 <MI2>  
A;Cross-references: EMBL:X82537; NID:g607176; PIDN:CAA57887.1; PID:g607178  
A;Experimental source: embryonic; brain  
A;Note: smaller form due to splicing  
C;Genetics:  
A;Introns: 125/3  
C;Superfamily: bcl apoptosis regulator, inhibitory type

Query Match 99.7%; Score 1214; DB 2; Length 233;  
Best Local Similarity 99.6%; Pred. No. 9.6e-99;  
Matches 232; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MSQSNRELVDVFLSYKLSQKYSWSQFSQSDVEENRTEAPEETEPEETPSAINGNPSWHLA	60
Db	1	MSQSNRELVDVFLSYKLSQKYSWSQFSQSDVEENRTEAPEETEPEETPSAINGNPSWHLA	60
Qy	61	DSPAVNGATGHSSSLDAREVPMAAVKQALREAGDEFELRYRRAFSDLTSLHTTPGTAY	120
Db	61	DSPAVNGATGHSSSLDAREVPMAAVKQALREAGDEFELRYRRAFSDLTSLHTTPGTAY	120
Qy	121	QSPFQVNNELFRDGVNNGRIVAFPSFGALCVESVDKEMQVLVSRIASWMTATYNDHLEP	180
Db	121	QSPFQVNNELFRDGVNNGRIVAFPSFGALCVESVDKEMQVLVSRIASWMTATYNDHLEP	180
Qy	181	WIQENGGWDTFVDLYGNNAAESKQGRFRNRFELTGMTVAGVLLGSLFSRK	233
Db	181	WIQENGGWDTFVDLYGNNAAESKQGRFRNRFELTGMTVAGVLLGSLFSRK	233

RESULT 2

I49056  
bcl-x long - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004

C;Accession: I49056; S52866  
R;Fang, W.; Rivard, J.J.; Mueller, D.L.; Behrens, T.W.  
J. Immunol. 153, 4388-4398, 1994  
A;Title: Cloning and molecular characterization of mouse bcl-x in B and T lymphocytes.  
A;Reference number: I49055; MUID:95052604; PMID:7963517  
A;Accession: I49056  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-233 <RES>  
A;Cross-references: UNIPROT:Q64373; EMBL:U10101; NID:G506647; PIDN:AAA82173.1; PID:G5066  
R;Kamesaki, H.; Michaud, G.Y.; Takatsu, K.; Okuma, M.  
Submitted to the EMBL Data Library, November 1994  
A;Description: IL-5 inhibits anti-IgM-induced apoptosis in an immature B cell line throu  
A;Reference number: S52866  
A;Accession: S52866  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-233 <KAW>  
A;Cross-references: EMBL:X83574; NID:G695622; PIDN:CAA58557.1; PID:G695623  
C;Superfamily: bcl apoptosis regulator, inhibitory type

Query Match 99.3%; Score 1210; DB 2; Length 233;  
Best Local Similarity 99.6%; Pred. No. 2.1e-98;  
Matches 232; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSQSNRELVDVFLSYKLSQKGSWSQFSDVEENRTEAPEETEPEETPSAINGNPSWHLA 60  
Db 1 MSQSNRELVDVFLSYKLSQKGSWSQFSDVEENRTEAPEETEPEETPSAINGNPSWHLA 60

Qy 61 DSPAVNGATGHSSSLDAREVPMVAVKQALREAGDEFEFLRYRRAFSDLTSLQHTTPTGAY 120  
Db 61 DSPAVNGATGHSSSLDAREVPMVAVKQALREAGDEFEFLRYRRAFSDLTSLQHTTPTGAY 120

Qy 121 QSFQVNVNELFRDGVNNGRIVAFPSFGGALCVESVDKEMQVLVSRIASWMTATYLNHLEP 180  
Db 121 QSFQVNVNELFRDGVNNGRIVAFPSFGGALCVESVDKEMQVLVSRIASWMTATYLNHLEP 180

Qy 181 WIQENGWDTFVDLYGNNAAESRKQGERFNRWFLTGMTVAGVLLGSLFSRK 233  
Db 181 WIQENGWDTFVDLYGNNAEAESRKQGERFNRWFLTGMTVAGVLLGSLFSRK 233

RESULT 3  
I67431  
BCL2-X-Long - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 09-Jul-2004  
C;Accession: I67431  
R;Tilly, J.L.; Tilly, K.I.; Kenton, M.L.; Johnson, A.L.  
Endocrinology 136, 232-241, 1995  
A;Title: Expression of members of the bcl-2 gene family in the immature rat ovary: equin  
onstitutive bcl-2 and bcl-x long messenger ribonucleic acid levels.  
A;Reference number: I53295; MUID:95129487; PMID:7828536  
A;Accession: I67431  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-233 <RES>  
A;Cross-references: UNIPROT:P53563; EMBL:U34963; NID:G1004376; PIDN:AAA77686.1; PID:G100  
C;Superfamily: bcl apoptosis regulator, inhibitory type

Query Match 97.5%; Score 1187; DB 2; Length 233;  
Best Local Similarity 97.4%; Pred. No. 2.2e-96;  
Matches 227; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MSQSNRELVDVFLSYKLSQKGSWSQFSDVEENRTEAPEETEPEETPSAINGNPSWHLA 60  
Db 1 MSQSNRELVDVFLSYKLSQKGSWSQFSDVEENRTEAPEETEPEETPSAINGNPSWHLA 60

Qy 61 DSPAVNGATGHSSSLDAREVPMVAVKQALREAGDEFEFLRYRRAFSDLTSLQHTTPTGAY 120  
Db 61 DSPAVNGATGHSSSLDAREVPMVAVKQALREAGDEFEFLRYRRAFSDLTSLQHTTPTGAY 120

Qy 121 QSFQVNVNELFRDGVNNGRIVAFPSFGGALCVESVDKEMQVLVSRIASWMTATYLNHLEP 180  
Db 121 QSFQVNVNELFRDGVNNGRIVAFPSFGGALCVESVDKEMQVLVSRIASWMTATYLNHLEP 180

Qy 181 WIQENGWDTFVDLYGNNAEAESRKQGERFNRWFLTGMTVAGVLLGSLFSRK 233  
Db 181 WIQENGWDTFVDLYGNNAEAESRKQGERFNRWFLTGMTVAGVLLGSLFSRK 233

Db 121 QSFQVNVNELFRDGVNNGRIVAFPSFGGALCVESVDKEMQVLVSRIASWMTATYLNHLEP 180

Qy 181 WIQENGWDTFVDLYGNNAEAESRKQGERFNRWFLTGMTVAGVLLGSLFSRK 233

Db 181 WIQENGWDTFVDLYGNNTAPESRKQGERFNRWFLTGMTVAGVLLGSLFSRK 233

RESULT 4  
B47537  
apoptosis regulator bcl-xL - human  
N;Alternate names: bcl-2-related protein  
N;Contains: apoptosis regulator bcl-xs  
C;Species: Homo sapiens (man)  
C;Date: 16-Aug-1996 #sequence\_revision 16-Aug-1996 #text\_change 09-Jul-2004  
C;Accession: B47537; C47537  
R;Boise, L.H.; Gonzalez-Garcia, M.; Postema, C.E.; Ding, L.; Lindsten, T.; Turka, L.A.;  
Cell 74, 597-608, 1993  
A;Title: bcl-x, a bcl-2-related gene that functions as a dominant regulator of apoptotic  
A;Reference number: A47537; MUID:93364977; PMID:8358789  
A;Accession: B47537  
A;Status: nucleic acid sequence not shown; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-233 <BOI>  
A;Cross-references: UNIPROT:Q07817; GB:L20121; NID:G510900; PIDN:CAA80661.1; PID:G510901  
A;Status: nucleic acid sequence not shown; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-69, 'G', 71-125, 189-233 <BO2>  
A;Cross-references: GB:L20122; NID:G623236; PIDN:CAA80662.1; PID:G623237  
C;Genetics:  
A;Gene: GDB:BCL2L  
A;Cross-references: GDB:228079  
C;Superfamily: bcl apoptosis regulator, inhibitory type  
C;Keywords: alternative splicing; apoptosis  
F;1-233/Product: apoptosis regulator bcl-xL #status predicted <MAT>  
F;1-125,189-233/Product: apoptosis regulator bcl-xs #status predicted <MA2>

Query Match 97.2%; Score 1184; DB 2; Length 233;  
Best Local Similarity 97.4%; Pred. No. 4e-96;  
Matches 227; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MSQSNRELVDVFLSYKLSQKGSWSQFSDVEENRTEAPEETEPEETPSAINGNPSWHLA 60  
Db 1 MSQSNRELVDVFLSYKLSQKGSWSQFSDVEENRTEAPEETEPEETPSAINGNPSWHLA 60

Qy 61 DSPAVNGATGHSSSLDAREVPMVAVKQALREAGDEFEFLRYRRAFSDLTSLQHTTPTGAY 120  
Db 61 DSPAVNGATGHSSSLDAREVPMVAVKQALREAGDEFEFLRYRRAFSDLTSLQHTTPTGAY 120

Qy 121 QSFQVNVNELFRDGVNNGRIVAFPSFGGALCVESVDKEMQVLVSRIASWMTATYLNHLEP 180  
Db 121 QSFQVNVNELFRDGVNNGRIVAFPSFGGALCVESVDKEMQVLVSRIASWMTATYLNHLEP 180

Qy 181 WIQENGWDTFVDLYGNNAEAESRKQGERFNRWFLTGMTVAGVLLGSLFSRK 233  
Db 181 WIQENGWDTFVDLYGNNAEAESRKQGERFNRWFLTGMTVAGVLLGSLFSRK 233

RESULT 5  
I49057  
bcl-x transmembrane deleted - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
C;Accession: I49057  
R;Fang, W.; Rivard, J.J.; Mueller, D.L.; Behrens, T.W.  
J. Immunol. 153, 4388-4398, 1994  
A;Title: Cloning and molecular characterization of mouse bcl-x in B and T lymphocytes.  
A;Reference number: I49055; MUID:95052604; PMID:7963517  
A;Accession: I49057  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-214 <RES>

A;Cross-references: UNIPROT:Q64373; EMBL:U10102; NID:9506649; PIDN:AAA82174.1; PID:950664  
C;Genetics:  
A;Gene: bcl-x-long  
C;Superfamily: bcl apoptosis regulator, inhibitory type

Query Match 82.6%; Score 1006; DB 2; Length 214;  
Best Local Similarity 99.5%; Pred. No. 1.3e-80;  
Matches 192; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSQSNRELVDVFLSYKLSQKGYSGWSQSDVEENRTEAPEETEPEERETPSAINGNPSWHLA 60  
Db 1 MSQSNRELVDVFLSYKLSQKGYSGWSQSDVEENRTEAPEETEPEERETPSAINGNPSWHLA 60

Qy 61 DSPAVNGATGHSSSLDAREVLPMAAVKQALREAGDEPELRYRRAFSDLTSQLHTTPGTAY 120  
Db 61 DSPAVNGATGHSSSLDAREVLPMAAVKQALREAGDEPELRYRRAFSDLTSQLHTTPGTAY 120

Qy 121 QSFQVNVNELFRDGVNNGRIVAFPSFGALCVESVDKEMQVLVSRIASWMTATYLNHLEP 180  
Db 121 QSFQVNVNELFRDGVNNGRIVAFPSFGALCVESVDKEMQVLVSRIASWMTATYLNHLEP 180

Qy 181 WIQENGWDVFD 193  
Db 181 WIQENGWDVFD 193

RESULT 6  
JE0203  
apoptosis regulator bcl-x isoform - human  
N;Alternate names: h-bcl-xbeta  
C;Species: Homo sapiens (man)  
C;Date: 21-Aug-1998 #sequence\_revision 21-Aug-1998 #text\_change 09-Jul-2004  
C;Accession: JE0203  
R;Ban, J.; Eckhart, L.; Weninger, W.; Mildner, M.; Tschachler, E.  
Biochem. Biophys. Res. Commun. 248, 147-152, 1998  
A;Title: Identification of a human cDNA encoding a novel bcl-x isoform.  
A;Reference number: JE0203; MUID:98340865; PMID:9675101  
A;Accession: JE0203  
A;Molecule type: mRNA  
A;Residues: 1-227 <BAN>  
A;Cross-references: UNIPROT:Q07817; GB:U72398; NID:g1622940; PIDN:AA817354.1; PID:g16229  
C;Genetics:  
A;Gene: bcl-x  
A;Map position: 20  
C;Superfamily: bcl apoptosis regulator, inhibitory type

Query Match 79.1%; Score 963; DB 2; Length 227;  
Best Local Similarity 97.9%; Pred. No. 8.3e-77;  
Matches 184; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MSQSNRELVDVFLSYKLSQKGYSGWSQSDVEENRTEAPEETEPEERETPSAINGNPSWHLA 60  
Db 1 MSQSNRELVDVFLSYKLSQKGYSGWSQSDVEENRTEAPEETEPEERETPSAINGNPSWHLA 60

Qy 61 DSPAVNGATGHSSSLDAREVLPMAAVKQALREAGDEPELRYRRAFSDLTSQLHTTPGTAY 120  
Db 61 DSPAVNGATGHSSSLDAREVLPMAAVKQALREAGDEPELRYRRAFSDLTSQLHTTPGTAY 120

Qy 121 QSFQVNVNELFRDGVNNGRIVAFPSFGALCVESVDKEMQVLVSRIASWMTATYLNHLEP 180  
Db 121 QSFQVNVNELFRDGVNNGRIVAFPSFGALCVESVDKEMQVLVSRIASWMTATYLNHLEP 180

Qy 181 WIQENGW 188  
Db 181 WIQENGW 188

RESULT 7  
I49055  
bcl-x short - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
C;Accession: I49055

R;Fang, W.; Rivard, J.J.; Mueller, D.L.; Behrens, T.W.  
J. Immunol. 153, 4388-4398, 1994  
A;Title: Cloning and molecular characterization of mouse bcl-x in B and T lymphocytes.  
A;Reference number: I49055; MUID:95052604; PMID:7963517  
A;Accession: I49055  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-170 <RES>  
A;Cross-references: UNIPROT:Q64373; EMBL:U10100; NID:9506645; PIDN:AAA82172.1; PID:950664  
C;Genetics:  
A;Gene: bcl-x  
C;Superfamily: bcl apoptosis regulator, inhibitory type

Query Match 67.8%; Score 825.5; DB 2; Length 170;  
Best Local Similarity 72.5%; Pred. No. 6e-65;  
Matches 169; Conservative 0; Mismatches 1; Indels 63; Gaps 1;

Qy 1 MSQSNRELVDVFLSYKLSQKGYSGWSQSDVEENRTEAPEETEPEERETPSAINGNPSWHLA 60  
Db 1 MSQSNRELVDVFLSYKLSQKGYSGWSQSDVEENRTEAPEETEPEERETPSAINGNPSWHLA 60

Qy 61 DSPAVNGATGHSSSLDAREVLPMAAVKQALREAGDEPELRYRRAFSDLTSQLHTTPGTAY 120  
Db 61 DSPAVNGATGHSSSLDAREVLPMAAVKQALREAGDEPELRYRRAFSDLTSQLHTTPGTAY 120

Qy 121 QSFQVNVNELFRDGVNNGRIVAFPSFGALCVESVDKEMQVLVSRIASWMTATYLNHLEP 180  
Db 121 QSFQVNVNELFRDGVNNGRIVAFPSFGALCVESVDKEMQVLVSRIASWMTATYLNHLEP 180

Qy 181 WIQENGWDVFDLYGNNAASERKGOERFNRWFLTGTGTAGVVLGSLFSRK 233  
Db 126 -----DTFVDLYGNNAASERKGOERFNRWFLTGTGTAGVVLGSLFSRK 170

RESULT 8  
I67435  
gene bcl-x short protein - rat (fragment)  
C;Species: Rattus sp. (rat)  
C;Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 28-Jul-2003  
C;Accession: I67435  
R;Tilly, J.L.; Tilly, K.I.; Kenton, M.L.; Johnson, A.L.  
Endocrinology 136, 232-241, 1995  
A;Title: Expression of members of the bcl-2 gene family in the immature rat ovary: equin  
onstitutive bcl-2 and bcl-x long messenger ribonucleic acid levels.  
A;Reference number: I53295; MUID:95129487; PMID:7828536  
A;Accession: I67435  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-176 <RES>  
A;Cross-references: GB:S78284; NID:g998483; PIDN:AA860702.1; PID:g998484  
C;Genetics:  
A;Gene: bcl-x  
C;Superfamily: bcl apoptosis regulator, inhibitory type

Query Match 67.2%; Score 818.5; DB 2; Length 176;  
Best Local Similarity 71.2%; Pred. No. 2.6e-64;  
Matches 166; Conservative 1; Mismatches 3; Indels 63; Gaps 1;

Qy 1 MSQSNRELVDVFLSYKLSQKGYSGWSQSDVEENRTEAPEETEPEERETPSAINGNPSWHLA 60  
Db 7 MSQSNRELVDVFLSYKLSQKGYSGWSQSDVEENRTEAPEETEPEERETPSAINGNPSWHLA 66

Qy 61 DSPAVNGATGHSSSLDAREVLPMAAVKQALREAGDEPELRYRRAFSDLTSQLHTTPGTAY 120  
Db 67 DSPAVNGATGHSSSLDAREVLPMAAVKQALREAGDEPELRYRRAFSDLTSQLHTTPGTAY 126

Qy 121 QSFQVNVNELFRDGVNNGRIVAFPSFGALCVESVDKEMQVLVSRIASWMTATYLNHLEP 180  
Db 127 QSFQVNVNELFRDGVNNGRIVAFPSFGALCVESVDKEMQVLVSRIASWMTATYLNHLEP 180

Qy 181 WIQENGWDVFDLYGNNAASERKGOERFNRWFLTGTGTAGVVLGSLFSRK 233  
Db 132 -----DTFVDLYGNNTAPESRKGOERFNRWFLTGTGTAGVVLGSLFSRK 176



A;Title: Analysis of the structure, transcripts, and protein products of bcl-2, the gene  
A;Reference number: A29409; MUID:86259760; PMID:3523487  
A;Accession: A29409  
A;Molecule type: mRNA  
A;Residues: 1-95,'A','G',111-236,'S','238-239 <TSU>  
A;Cross-references: GB:M1394; NID:g179366; PIDN:AAA51813.1; PID:g179367  
A;Note: this sequence has been corrected in reference A3732  
R;Seto, M.; Jaeger, U.; Hockett, R.D.; Graninger, W.; Bennett, S.; Goldman, P.; Korsmeyer,  
EMBO J. 7, 123-131, 1988  
A;Title: Alternative promoters and exons, somatic mutation and deregulation of the Bcl-2  
A;Reference number: S02452; MUID:88196071; PMID:2834197  
A;Accession: S02452  
A;Molecule type: mRNA  
A;Residues: 1-239 <SET>  
R;Cleary, M.L.; Smith, R.A.; Sklar, J.  
Cell 47, 19-28, 1986  
A;Title: Cloning and structural analysis of cDNAs for bcl-2 and a hybrid bcl-2/immunoglobulin  
A;Reference number: A24428; MUID:87002488; PMID:2875799  
A;Accession: A24428  
A;Molecule type: mRNA  
A;Residues: 1-58,'T','60-116,'R',118-239 <CLE>  
A;Cross-references: GB:M14745; NID:g179370; PIDN:AAA35591.1; PID:g179371  
R;Hua, C.; Zorn, S.; Jensen, J.P.; Coupland, R.W.; Ko, H.S.; Wright, J.J.; Bakshi, A.  
Oncogene Res. 2, 263-275, 1988  
A;Title: Consequences of the t(14;18) chromosomal translocation in follicular lymphoma:  
A;Reference number: A27622; MUID:88217344; PMID:3285301  
A;Accession: A27622  
A;Molecule type: mRNA  
A;Residues: 1-58,'T','60-239 <HUA>  
A;Accession: B27622  
A;Molecule type: DNA  
A;Residues: 1-6,'S','8-58,'T','60-128,'C',130-239 <HUA2>  
A;Note: the sequence was determined from the germline gene  
C;Comment: Constitutive expression of BCL2 following t(14;18) chromosomal translocation  
C;Genetics:  
A;Gene: GDB:BCL2  
A;Cross-references: GDB:l119031; OMIM:151430  
A;Map position: 18q21.3-18q21.3  
C;Function:  
C;Superfamily: bcl apoptosis regulator, inhibitory type  
C;Keywords: alternative splicing; apoptosis; B-cell lymphoma; follicular lymphoma; proto

Query Match 38.1%; Score 464; DB 1; Length 239;  
Best Local Similarity 44.5%; Pred. No. 4e-33;  
Matches 106; Conservative 30; Mismatches 68; Indels 34; Gaps 8;

QY 5 NRELVDVFLSKLSQKYSWQSFDVENRTTEAPEETEPTPSAINGNPSW--HLADS 62  
|||::: : |||||::| | | | | | | | | | | | | | | | | | | | | |  
Db 11 NRBITVMKYIHYKLRSQGYEWDA-GDV-----GAAPPQAAP---APGIFSSQPCHTPHPAAS 62  
  
QY 63 -----PAVNGATGHSSSLDAREVIPMAAVKQALREAGDEFELRYRAFSDLTS 110  
|||::: : |||||::| | | | | | | | | | | | | | | | | | | | | |  
Db 63 RDVPARTSPQTAPAAGA-----AAAGPALSPPV-PVVHLTLRQAGDDFSRRYRDFAEMSS 117  
  
QY 111 QLHLTPGTAYQSFPQQVNELEFRDGVNWGRIVAFPSFGGALCVESVDKMQVLVSRIASWM 170  
118 QLHLTPGTARGFATTVVEELFRDGVNWGRIVAFPEFGGVWCVCVESVNREMSPLVDNIALLWM 177  
  
QY 171 ATYLNDHLEPMIQNGGWDTTFVDLYGNNAABSRKGQERFNRFWTGCMTVAGVVLLGS 228  
|||::: : |||||::| | | | | | | | | | | | | | | | | | | | | |  
Db 178 TEYLNRHLHTWIQDGGWDADFVELYGPSM-----RPLDFDSWLSTLILLALVGA 228

RESULT 15  
153744  
gene bcl-2 protein - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 09-Jul-2004  
C;Accession: I53744  
R;Sato, T.; Irie, S.; Krajewski, S.; Reed, J.C.  
Gene 140, 291-292, 1994  
A;Title: Cloning and sequencing of a cDNA encoding the rat Bcl-2 protein

A;Reference number: I53744; MUID:94193015; PMID:8144041  
A;Accession: I53744  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-236 <RES>  
A;Cross-references: UNIPROT:P49950; GB:L14680; NID:g408946; PIDN:AAA53662.1; PID:g408947  
C;Genetics:  
A;Gene: bcl-2  
C;Superfamily: bcl apoptosis regulator, inhibitory type

Query Match 37.8%; Score 460.5; DB 2; Length 236;  
Best Local Similarity 43.4%; Pred. NO. 7.9e-33;  
Matches 102; Conservative 34; Mismatches 68; Indels 31; Gaps 6;

Qy 5 NRELVDPLSYKLSQKGYSMQSFSDVENRTEAPEETEPEP--ETPSAINGNPSWHLADS 62  
Db 11 NREIVMKYIHVKLSQSGYEW-----TGDEDSAPLRAAPTGGIFSQPESN--RT 58  
Qy 63 PAVNGATGHSSSLDAREVIPMA-----AVKQALREAGDEPELRYRRAPFSDLTSLH 113  
Db 59 PAVHRDTAARTS-PLRPLVANAGPALSPVPVHLLTRAGDDPSRRYRRDFAEMSSQLH 117  
Qy 114 ITPGTAYQSFQVNNELFRDGVNMGRIIVAFPSFGALCVESVDKEMQVLSRIASWMATY 173  
Db 118 LTPFTARGRFATVVEELFRDGVNMGRIIVAFPEFGGVMCGSVNREMSPLVDNIALMMTEY 177  
Qy 174 LNDHLEPMIOENGWDTFVDLYGNNAAESRKQERFNRWFLTGMTVAGVVLLGS 228  
Db 178 LNRHLHTWIQDNGGWDAFVELYGPSM-----RPLDFSWLSLKTLLSLALVGA 225

Search completed: March 31, 2005, 00:31:34  
Job time : 32.4692 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 31, 2005, 00:25:06 ; Search time 112.019 Seconds  
(without alignments)  
688.690 Million cell updates/sec

Title: US-10-049-822a-2  
Perfect score: 1218  
Sequence: 1 MSQSNRELVDFLSYKLSQK.....FLTGMTVAGVLLGSLFSRK 233

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1407402 seqs, 331100923 residues

Total number of hits satisfying chosen parameters: 1407402

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:  
1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
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9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep.\*  
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11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*  
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13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep.\*  
17: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*  
19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*  
20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	1196	98.2	233	15	US-10-402-017-4
2	1190	97.7	233	14	US-10-101-482-14
3	1184	97.2	233	9	US-09-734-846-2
4	1184	97.2	233	9	US-09-952-278-6
5	1184	97.2	233	14	US-10-072-830-4
6	1184	97.2	233	14	US-10-169-223-10
7	1184	97.2	233	14	US-10-302-262-2
8	1184	97.2	233	15	US-10-116-275-171
9	1184	97.2	233	16	US-10-450-366-5
10	1184	97.2	233	16	US-10-659-705-8
11	1184	97.2	411	16	US-10-792-517-2
12	1090	89.5	219	15	US-10-402-017-10
13	1079	88.6	219	15	US-10-402-017-12

14	1075	88.3	212	14	US-10-169-223-14	Sequence 14, Appl
15	1061	87.1	485	16	US-10-792-517-8	Sequence 8, Appl
16	979	80.4	235	14	US-10-208-155-2	Sequence 2, Appl
17	967	79.4	199	15	US-10-402-017-8	Sequence 8, Appl
18	949	77.9	185	9	US-09-864-761-40954	Sequence 40954, A
19	917	75.3	229	16	US-10-659-705-7	Sequence 7, Appl
20	866	71.1	179	15	US-10-402-017-6	Sequence 6, Appl
21	808.5	66.4	170	15	US-10-003-632C-7	Sequence 7, Appl
22	802.5	65.9	170	9	US-09-952-278-8	Sequence 8, Appl
23	751	61.7	152	14	US-10-158-769-2	Sequence 2, Appl
24	732	60.1	190	9	US-09-952-278-2	Sequence 2, Appl
25	588	48.3	237	16	US-10-659-705-5	Sequence 5, Appl
26	515.5	42.3	204	16	US-10-659-705-6	Sequence 6, Appl
27	488	40.1	233	16	US-10-659-705-3	Sequence 3, Appl
28	464	38.1	239	14	US-10-277-693A-10	Sequence 10, Appl
29	464	38.1	239	15	US-10-003-632C-10	Sequence 10, Appl
30	464	38.1	239	15	US-10-003-632C-13	Sequence 13, Appl
31	461	37.8	239	8	US-08-726-211-5	Sequence 5, Appl
32	461	37.8	239	10	US-09-993-420A-8	Sequence 8, Appl
33	461	37.8	239	14	US-10-101-482-12	Sequence 12, Appl
34	461	37.8	239	14	US-10-072-830-2	Sequence 2, Appl
35	461	37.8	239	14	US-10-141-618-12	Sequence 12, Appl
36	461	37.8	239	14	US-10-053-645A-21	Sequence 21, Appl
37	461	37.8	239	15	US-10-387-961A-5	Sequence 5, Appl
38	461	37.8	239	15	US-10-003-632C-1	Sequence 1, Appl
39	461	37.8	239	15	US-10-003-632C-3	Sequence 3, Appl
40	461	37.8	239	15	US-10-148-953A-1	Sequence 1, Appl
41	461	37.8	239	16	US-10-450-366-4	Sequence 4, Appl
42	461	37.8	239	16	US-10-770-668-16	Sequence 16, Appl
43	458.5	37.6	236	13	US-10-087-192-1953	Sequence 1953, Ap
44	458	37.6	239	15	US-10-148-953A-2	Sequence 2, Appl
45	458	37.6	239	15	US-10-148-953A-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1

US-10-402-017-4  
; Sequence 4, Application US/10402017  
; Publication No. US20030219871A1  
; GENERAL INFORMATION: Heiko MEENTIS and Martin FUSSENEGGER  
; APPLICANT: Barbara ENENKEL, Host cells having improved survival properties and methods to gen  
; TITLE OF INVENTION: such cells  
; FILE REFERENCE: Case 1/1314  
; CURRENT APPLICATION NUMBER: US/10/402,017  
; CURRENT FILING DATE: 2003-03-28  
; PRIOR APPLICATION NUMBER: US 60/369,307  
; PRIOR APPLICATION NUMBER: April 2, 2002  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 233  
; TYPE: PRT  
; ORGANISM: Cricetus griseus  
US-10-402-017-4

Query Match	98.2%	Score	1196	DB	15	Length	233
Best Local Similarity	98.3%	Pred. No.	6.7e-111	Mismatches	2	Indels	0
Matches	229	Conservative	2	Gaps	0		
Qy	1	MSQSNRELVDFLSYKLSQKYSWSQSDVEENRTEAPEETEPEPTPSAINGNPSMHLA	60				
Db	1	MSQSNRELVDFLSYKLSQKYSWSQSDVEENRTEAPEETEPEPTPSAINGNPSMHLA	60				
Qy	61	DSPAVNGATGHSSSLDAREVIPMAAVKALREAGDEFEELRYRRFSDLTSLQHTPGTAY	120				
Db	61	DSPAVNGATGHSSSLDAREVIPMAAVKALREAGDEFEELRYRRFSDLTSLQHTPGTAY	120				
Qy	121	QSFQVNVNLFPRDGVNNGRIVAFPSFGALCVESVDKEMQVLVSRIASMATYLNHLEP	180				
Db	121	QSFQVNVNLFPRDGVNNGRIVAFPSFGALCVESVDKEMQVLVSRIASMATYLNHLEP	180				

Qy 181 WIQENGWDTFVDLYGNNAAESRKQGRFNRWFLTGMTVAGVLLGSLFSRK 233  
Db 181 WIQENGWDTFVELYGNNAAESRKQGRFNRWFLTGMTVAGVLLGSLFSRK 233

RESULT 2  
US-10-101-482-14  
; Sequence 14, Application US/10101482  
; Publication No. US2003000837A1  
; GENERAL INFORMATION:  
; APPLICANT: KIEFER, MICHAEL C.  
; BARR, PHILIP J.  
; TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA  
; ENCODING THE PROTEINS AND METHODS OF USE THEREOF  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 Page Mill Road  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/101,482  
; FILING DATE: 18-Mar-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/320,157  
; FILING DATE: 07-OCT-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: LEHNHARDT, SUSAN K.  
; REGISTRATION NUMBER: 33,943  
; REFERENCE/DOCKET NUMBER: 23647-20007.20  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 813-5600  
; TELEFAX: (415) 494-0792  
; TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 233 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:  
US-10-101-482-14

Query Match 97.7%; Score 1190; DB 14; Length 233;  
Best Local Similarity 97.9%; Pred. No. 2.7e-110;  
Matches 228; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MSQSNRELVDPLSYKLSQKGYNSQFSDVEENRTEAPEETEPEPTPSAINGNPSWHLA 60  
Db 1 MSQSNRELVDPLSYKLSQKGYNSQFSDVEENRTEAPEETEPEPTPSAINGNPSWHLA 60

Qy 61 DSPAVNGATGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHTPGTAY 120  
Db 61 DSPAVNGATGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHTPGTAY 120

Qy 121 QSFQVYNELFRDGVNNGRIVAFPSFGGALCVESVDKEMQVLVSRIASWMATYLNHLEP 180  
Db 121 QSFQVYNELFRDGVNNGRIVAFPSFGGALCVESVDKEMQVLVSRIASWMATYLNHLEP 180

Qy 181 WIQENGWDTFVDLYGNNAAESRKQGRFNRWFLTGMTVAGVLLGSLFSRK 233  
Db 181 WIQENGWDTFVELYGNNAAESRKQGRFNRWFLTGMTVAGVLLGSLFSRK 233

RESULT 3  
US-09-734-846-2  
; Sequence 2, Application US/09734846  
; Patent No. US20010007025A1  
; GENERAL INFORMATION:  
; APPLICANT: Bennett, C. Frank  
; APPLICANT: Dean, Nicholas M.  
; APPLICANT: Monia, Brett P.  
; APPLICANT: Nickoloff, Brian J.  
; APPLICANT: Zhang, Qingqing  
; TITLE OF INVENTION: Antisense Modulation of bcl-x Expression  
; FILE REFERENCE: ISPH-0528  
; CURRENT APPLICATION NUMBER: US/09/734,846  
; CURRENT FILING DATE: 2000-12-12  
; PRIOR APPLICATION NUMBER: 09/277,020  
; PRIOR FILING DATE: 1998-03-26  
; PRIOR APPLICATION NUMBER: 09/167,921  
; PRIOR FILING DATE: 1998-10-07  
; PRIOR APPLICATION NUMBER: 09/323,743  
; PRIOR FILING DATE: 1999-06-02  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 233  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-734-846-2

Query Match 97.2%; Score 1184; DB 9; Length 233;  
Best Local Similarity 97.4%; Pred. No. 1.1e-109;  
Matches 227; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MSQSNRELVDPLSYKLSQKGYNSQFSDVEENRTEAPEETEPEPTPSAINGNPSWHLA 60  
Db 1 MSQSNRELVDPLSYKLSQKGYNSQFSDVEENRTEAPEETEPEPTPSAINGNPSWHLA 60

Qy 61 DSPAVNGATGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHTPGTAY 120  
Db 61 DSPAVNGATGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHTPGTAY 120

Qy 121 QSFQVYNELFRDGVNNGRIVAFPSFGGALCVESVDKEMQVLVSRIASWMATYLNHLEP 180  
Db 121 QSFQVYNELFRDGVNNGRIVAFPSFGGALCVESVDKEMQVLVSRIASWMATYLNHLEP 180

Qy 181 WIQENGWDTFVDLYGNNAAESRKQGRFNRWFLTGMTVAGVLLGSLFSRK 233  
Db 181 WIQENGWDTFVELYGNNAAESRKQGRFNRWFLTGMTVAGVLLGSLFSRK 233

RESULT 4  
US-09-952-278-6  
; Sequence 6, Application US/09952278  
; Patent No. US20020137182A1  
; GENERAL INFORMATION:  
; APPLICANT: Thompson, Craig B.  
; ; Boise, Lawrence H.  
; TITLE OF INVENTION: Vertebrate Apoptosis Gene:  
; Compositions and Methods  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: 321 No. US20020137182A1th Clark Street, Suite 800  
; CITY: Chicago  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60610  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/952,278

```
; FILING DATE: 12-Sep-2001
; CLASSIFICATION: <Unknown>
; PRIORITY: 1
; APPLICATION NUMBER: US/08/081,448
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
;   NAME: No. US20020137182Althrup, Thomas E.
;   REGISTRATION NUMBER: 33,268
;   REFERENCE/DOCKET NUMBER: ARCD090
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 312-744-0090
;   TELEFAX: 312-755-4489
; INFORMATION FOR SEQ ID NO: 6:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 233 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-952-278-6

Query Match          97.2%; Score 1184; DB 9; Length 233;
Best Local Similarity 97.4%; Pred. No. 1.1e-109;
Matches 227; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MSQSNRELVDVFLSYKLSQKGYSSQFSDVEENRTEAPEETEPEPTPSAINGNPSWHLA 60
Db 1 MSQSNRELVDVFLSYKLSQKGYSSQFSDVEENRTEAPEETEPEPTPSAINGNPSWHLA 60

Qy 61 DSPAVNGATGHSSSLDAREVIPAQAQALREAGDEFELELYRRRAFSDLTSLQHTTPGTAY 120
Db 61 DSPAVNGATGHSSSLDAREVIPAQAQALREAGDEFELELYRRRAFSDLTSLQHTTPGTAY 120

Qy 121 QSEFQVNVNELFRDGVNMGRIIVAFPSFGALCVESVDKEMQVLSRIASWMTATYLNHLEP 180
Db 121 QSEFQVNVNELFRDGVNMGRIIVAFPSFGALCVESVDKEMQVLSRIASWMTATYLNHLEP 180

Qy 181 WIOENGGWDTFVDLYGNNAAESRKQGRFNRNFWLTGMTVAGVVLGSLFSRK 233
Db 181 WIOENGGWDTFVDLYGNNAAESRKQGRFNRNFWLTGMTVAGVVLGSLFSRK 233

RESULT 6
US-10-169-223-10
; Sequence 10, Application US/10169223
; Publication No. US20030152946A1
; GENERAL INFORMATION:
; APPLICANT: SHIMIZU, Shigeomi
; APPLICANT: TSUBIMOTO, Yoshihide
; TITLE OF INVENTION: BH4-Fused Polypeptides
; FILE REFERENCE: 1422-0537P
; CURRENT APPLICATION NUMBER: US/10/169,223
; CURRENT FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: JP 11-371449
; PRIOR FILING DATE: 1999-12-27
; PRIOR APPLICATION NUMBER: PCT/JP00/09274
; PRIOR FILING DATE: 2000-12-26
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-169-223-10

Query Match          97.2%; Score 1184; DB 14; Length 233;
Best Local Similarity 97.4%; Pred. No. 1.1e-109;
Matches 227; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MSQSNRELVDVFLSYKLSQKGYSSQFSDVEENRTEAPEETEPEPTPSAINGNPSWHLA 60
Db 1 MSQSNRELVDVFLSYKLSQKGYSSQFSDVEENRTEAPEETEPEPTPSAINGNPSWHLA 60

Qy 61 DSPAVNGATGHSSSLDAREVIPAQAQALREAGDEFELELYRRRAFSDLTSLQHTTPGTAY 120
Db 61 DSPAVNGATGHSSSLDAREVIPAQAQALREAGDEFELELYRRRAFSDLTSLQHTTPGTAY 120

Qy 121 QSEFQVNVNELFRDGVNMGRIIVAFPSFGALCVESVDKEMQVLSRIASWMTATYLNHLEP 180
Db 121 QSEFQVNVNELFRDGVNMGRIIVAFPSFGALCVESVDKEMQVLSRIASWMTATYLNHLEP 180

Qy 181 WIOENGGWDTFVDLYGNNAAESRKQGRFNRNFWLTGMTVAGVVLGSLFSRK 233
Db 181 WIOENGGWDTFVDLYGNNAAESRKQGRFNRNFWLTGMTVAGVVLGSLFSRK 233

RESULT 7
US-10-302-262-2
; Sequence 2, Application US/10302262
; Publication No. US20030191300A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Monia, Brett P.
; APPLICANT: Nickoloff, Brian J.
; APPLICANT: Zhang, Qingqing
; TITLE OF INVENTION: Antisense Modulation of bcl-x Expression
```

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; FILE REFERENCE: ISPH-0528
; CURRENT APPLICATION NUMBER: US/10/302,262
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/09/734,846
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 09/277,020
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 09/167,921
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 09/323,743
; PRIOR FILING DATE: 1999-06-02
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-302-262-2

```

Query Match	97.2%;	Score 1184;	DB 14;	Length 233;
Best Local Similarity	97.4%;	Pred. No. 1.1e-109;		
Matches 227;	Conservative	2;	Mismatches 4;	Indels 0; Gaps 0
QY	1	MSQSRELVDVFLSKLQKSGYSQSDVEENTEAPEETEPEETPSAINGNSWHLA	60	
Db	1	MSQSRELVDVFLSKLQKSGYSQSDVEENTEAPEETEPEETPSAINGNSWHLA	60	
QY	61	DSPAVNGATGHSSSLDAREVTPMAAVKQALREAGDEFELRYRAFDLSLTQSLHITPGTAY	120	
Db	61	DSPAVNGATAHSSSLDAREVTPMAAVKQALREAGDEFELRYRAFDLSLTQSLHITPGTAY	120	
QY	121	QSFQVNNELFRDGNWNGRIIVAFPSFGALCVESVDKEMQVLSRTASNMATVYLNHLEP	180	
Db	121	QSFQVNNELFRDGNWNGRIIVAFPSFGALCVESVDKEMQVLSRTASNMATVYLNHLEP	180	
QY	181	WIQENGMDTFVDLYGNNAAEESRKQGERFNRNFWLTGMTVAGVVLGSLFSRK	233	
Db	181	WIQENGMDTFVELYGNNAAEESRKQGERFNRNFWLTGMTVAGVVLGSLFSRK	233	

```

RESULT 8
US-10-116-275-171
; Sequence 171, Application US/10116275
; Publication No. US20030211476A1
; GENERAL INFORMATION:
; APPLICANT: Elan Pharmaceutical Technology
; APPLICANT: O'Mahony, Daniel J.
; APPLICANT: Brayden, David
; APPLICANT: Byrne, Daragh
; APPLICANT: Lambkin, Imelda
; APPLICANT: Higgins, Lisa
; TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and M Cells and Methods and
; TITLE OF INVENTION: Compositions Targeting Peyer's Patches and M Cell Receptors
; FILE REFERENCE: E1067/20087
; CURRENT APPLICATION NUMBER: US/10/116,275
; CURRENT FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 171
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-116-275-171

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	Query Match	97.2%	Score 1184;	DB 15;	Length 233;
	Best Local Similarity	97.4%;	Pred. No. 1.1e-109;		
	Matches 227; Conservative	2;	Mismatches 4;	Indels	0; Gaps 0;
Qy	1 MSQSNRELVDVDFLYKLSQKGYSQSQFSDVEENRTEAPEPEPRRTPSAINGNP	60			
Db	1 MSQSNRELVDVDFLYKLSQKGYSQSQFSDVEENRTEAPEPEGESEMETPSAINGNP	60			
Dv	61 DSPAVNCATGCHSSSIDAREVTPMAA VKOALFEAGDEFLRYRRAFSDITSLSHITPGTAY	120			

Db	61	DS	PA	VG	AT	AH	SS	SL	DA	RE	VI	PM	AA	VQ	AL	FE	AG	DE	FE	LY	RR	AF	SD	UT	SQ	HT	PG	TA	120	
Qy	121	QS	FE	QV	VN	NEL	FR	DG	VN	NG	R	VA	PF	PS	FG	CA	LC	VE	SD	KEM	QV	LS	RI	AS	WM	AT	YLN	DH	LE	180
Db	121	QS	FE	QV	VN	NEL	FR	DG	VN	NG	R	VA	PF	PS	FG	CA	LC	VE	SD	KEM	QV	LS	RI	AS	WM	AT	YLN	DH	LE	180
Qy	181	WI	QNG	GW	DT	FV	DL	Y	GN	AA	AE	SK	GO	ER	FN	RW	FL	TG	MT	VA	GV	VL	GL	SF	GR	233				
Db	181	WI	QNG	GW	DT	FV	DL	Y	GN	AA	AE	SK	GO	ER	FN	RW	FL	TG	MT	VA	GV	VL	GL	SF	GR	233				

```

RESULT 9
US-10-450-366-5
; Sequence 5, Application US/10450366
; Publication No. US20040115667A1
; GENERAL INFORMATION:
; APPLICANT: Tschopp, Jorg
; APPLICANT: Hoffmann, Kay
; TITLE OF INVENTION: DNA-Sequences, which
; FILE REFERENCE: 11436*3
; CURRENT APPLICATION NUMBER: US/10/450,366
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: PCT/EP01/14597
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: DE 100 61 766.2
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: DE 101 00 280.7
; PRIOR FILING DATE: 2001-01-04
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Human Bcl-XL
US-10-450-366-5

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Query Match          97.2%; Score 1184; DB 16; Length 233;
Best Local Similarity 97.4%; Pred. No. 1.1e-109;
Matches 227; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy      1  MSQSNRELVDLFSLYKLSQKGYSWQSFSDVEENRTEAPEBETPEPETAINGNPWSHLA 60
Db      1  MSQSNRELVDLFSLYKLSQKGYSWQSFSDVEENRTEAPEGTESEMETPSAINGNPWSHLA 60

Qy     61  DSPAVNGATGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHTPGTAY 120
Db     61  DSPAVNGATAHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHTPGTAY 120

Qy    121  QSPFQVNNELPRGVNNGRIVAFPSFGGALCVESVDKEMQVLVSRIASWATYLNHLEP 180
Db    121  QSPFQVNNELPRGVNNGRIVAFPSFGGALCVESVDKEMQVLVSRIASWATYLNHLEP 180

Qy    181  WIQENGWDTFVDLYGNNAEAERKGOERNRWFPLTGMTVAGVVLGSLFSRK 233
Db    181  WIQENGWDTFVELYGNNAEAERKGOERNRWFPLTGMTVAGVVLGSLFSRK 233

RESULT 10
US-10-659-705-8
; Sequence 8, Application US/10659705
; Publication No. US20040117867A1
; GENERAL INFORMATION:
; APPLICANT: Look, A. Thomas
; APPLICANT: Langenau, David M.
; TITLE OF INVENTION: Transgenic Cancer Models in Fish
; FILE REFERENCE: 112706.123
; CURRENT APPLICATION NUMBER: US/10/659,705
; PRIORITY FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 60/409,585
; PRIOR FILING DATE: 2002-09-11

```

NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 233  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: BCL2 proteins  
US-10-659-705-8

Query Match 97.2%; Score 1184; DB 16; Length 233;  
Best Local Similarity 97.4%; Pred. No. 1.1e-109;  
Matches 227; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
  
Qy 1 MSQSNRELVDPLSYKLSQKGYSSQFSDVEENRTEAPEETEPEPTPSAINGNPSWHLA 60  
Db 1 MSQSNRELVDPLSYKLSQKGYSSQFSDVEENRTEAPEETEPEPTPSAINGNPSWHLA 60  
  
Qy 61 DSPAVNGATGHSSSLDAREVIPMAAVKQALREAGDEFEELRYRRAPSDLTSQLHTTPGTAY 120  
Db 61 DSPAVNGATGHSSSLDAREVIPMAAVKQALREAGDEFEELRYRRAPSDLTSQLHTTPGTAY 120  
  
Qy 121 QSFEQVNNELFRDGVNNGRIVAFPSFGGALCVESVDKEMQVLVSRIASWMTATYLNHLEP 180  
Db 121 QSFEQVNNELFRDGVNNGRIVAFPSFGGALCVESVDKEMQVLVSRIASWMTATYLNHLEP 180  
  
Qy 181 WIQENGWDTTFVDLYGNNAAESRKQGRFNRNFWLTGMTVAGVLLGSLFSRK 233  
Db 181 WIQENGWDTTFVDLYGNNAAESRKQGRFNRNFWLTGMTVAGVLLGSLFSRK 233

RESULT 11  
US-10-792-517-2  
; Sequence 2, Application US/10792517  
; Publication No. US20040152179A1  
; GENERAL INFORMATION:  
; APPLICANT: Youle et al.  
; TITLE OF INVENTION: RECEPTOR-MEDIATED UPTAKE OF AN EXTRACELLULAR BCL-XL  
; FILE REFERENCE: 4239-55417  
; CURRENT APPLICATION NUMBER: US/10/792,517  
; CURRENT FILING DATE: 2004-03-02  
; PRIOR APPLICATION NUMBER: US/09/639,245  
; PRIOR FILING DATE: 2000-08-15  
; PRIOR APPLICATION NUMBER: 60/149,220  
; PRIOR FILING DATE: 1999-08-16  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 411  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: genetic fusion  
US-10-792-517-2

Query Match 97.2%; Score 1184; DB 16; Length 411;  
Best Local Similarity 97.4%; Pred. No. 2.3e-109;  
Matches 227; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
  
Qy 1 MSQSNRELVDPLSYKLSQKGYSSQFSDVEENRTEAPEETEPEPTPSAINGNPSWHLA 60  
Db 21 MSQSNRELVDPLSYKLSQKGYSSQFSDVEENRTEAPEETEPEPTPSAINGNPSWHLA 80  
  
Qy 61 DSPAVNGATGHSSSLDAREVIPMAAVKQALREAGDEFEELRYRRAPSDLTSQLHTTPGTAY 120  
Db 81 DSPAVNGATGHSSSLDAREVIPMAAVKQALREAGDEFEELRYRRAPSDLTSQLHTTPGTAY 140  
  
Qy 121 QSFEQVNNELFRDGVNNGRIVAFPSFGGALCVESVDKEMQVLVSRIASWMTATYLNHLEP 180  
Db 141 QSFEQVNNELFRDGVNNGRIVAFPSFGGALCVESVDKEMQVLVSRIASWMTATYLNHLEP 200  
  
Qy 181 WIQENGWDTTFVDLYGNNAAESRKQGRFNRNFWLTGMTVAGVLLGSLFSRK 233

Db 201 WIQENGWDTTFVDLYGNNAAESRKQGRFNRNFWLTGMTVAGVLLGSLFSRK 253  
  
RESULT 12  
US-10-402-017-10  
; Sequence 10, Application US/10402017  
; Publication No. US20030219871A1  
; GENERAL INFORMATION:  
; APPLICANT: Barbara ENENKEL, Heiko MEENTS and Martin FUSSENEGGER  
; TITLE OF INVENTION: Host cells having improved survival properties and methods to gen  
; FILE REFERENCE: Case 1/1314  
; CURRENT APPLICATION NUMBER: US/10/402,017  
; CURRENT FILING DATE: 2003-03-28  
; PRIOR APPLICATION NUMBER: US 60/369,307  
; PRIOR APPLICATION NUMBER: April 2, 2002  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 10  
; LENGTH: 219  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Deletion mutant of SEQ ID NO:4 (del166-83)  
US-10-402-017-10

Query Match 89.5%; Score 1090; DB 15; Length 219;  
Best Local Similarity 91.0%; Pred. No. 2.4e-100;  
Matches 212; Conservative 2; Mismatches 5; Indels 14; Gaps 1;  
  
Qy 1 MSQSNRELVDPLSYKLSQKGYSSQFSDVEENRTEAPEETEPEPTPSAINGNPSWHLA 60  
Db 1 MSQSNRELVDPLSYKLSQKGYSSQFSDVEENRTEAPEETEPEPTPSAINGNPSWHLA 60  
  
Qy 61 DSPAVNGATGHSSSLDAREVIPMAAVKQALREAGDEFEELRYRRAPSDLTSQLHTTPGTAY 120  
Db 61 DSPAVNGATGHSSSLDAREVIPMAAVKQALREAGDEFEELRYRRAPSDLTSQLHTTPGTAY 106  
  
Qy 121 QSFEQVNNELFRDGVNNGRIVAFPSFGGALCVESVDKEMQVLVSRIASWMTATYLNHLEP 180  
Db 107 QSFEQVNNELFRDGVNNGRIVAFPSFGGALCVESVDKEMQVLVSRIASWMTATYLNHLEP 166  
  
Qy 181 WIQENGWDTTFVDLYGNNAAESRKQGRFNRNFWLTGMTVAGVLLGSLFSRK 233  
Db 167 WIQENGWDTTFVDLYGNNAAESRKQGRFNRNFWLTGMTVAGVLLGSLFSRK 219

RESULT 13  
US-10-402-017-12  
; Sequence 12, Application US/10402017  
; Publication No. US20030219871A1  
; GENERAL INFORMATION:  
; APPLICANT: Barbara ENENKEL, Heiko MEENTS and Martin FUSSENEGGER  
; TITLE OF INVENTION: Host cells having improved survival properties and methods to gen  
; FILE REFERENCE: Case 1/1314  
; CURRENT APPLICATION NUMBER: US/10/402,017  
; CURRENT FILING DATE: 2003-03-28  
; PRIOR APPLICATION NUMBER: US 60/369,307  
; PRIOR APPLICATION NUMBER: April 2, 2002  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 12  
; LENGTH: 219  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Deletion mutant of SEQ ID NO:4 (del126-83)  
US-10-402-017-12

Query Match 88.6%; Score 1079; DB 15; Length 219;  
Best Local Similarity 91.0%; Pred. No. 3e-99;

Matches	212; Conservative	3; Mismatches	4; Indels	14; Gaps	1;
Qy	1	MSQSNRELVDVDFLSYKLSQKGYWSQSFSDVEENRTEAPEETEPETPSAINGNPSWHLA	60		
Db	1	MSQSNRELVDVDFLSYKLSQKGYWSQSFSDVEENRTEAPEGTESR	-----A	46	
Qy	61	DSFAVNGATGCHSSSLDAREVIPMAAVKQALREAGDEFELYRRRAFSDLTSQLHTPGTAY	120		
		:			
Db	47	AAAAVNGATGCHSSSLDAREVIPMAAVKQALREAGDEFELYRRRAFSDLTSQLHTPGTAY	106		
Qy	121	QSFQVNVNELFRDGVNNGRIVAPPSFGALCVESVDKEMQVLSRIASWATYLNDLHLEP	180		
Db	107	QSFQVNVNELFRDGVNNGRIVAPPSFGALCVESVDKEMQVLSRIASWATYLNDLHLEP	166		
Qy	181	WIQENGWDFTVDLYGNNAAESKGGERNRWF LTGWTAGVGVLLGSLFSRK	233		
Db	167	WIQENGWDFTVELYGNNAAESKGGERNRWF LTGWTAGVGVLLGSLFSRK	219		

```

RESULT 14
US-10-169-223-14
; Sequence 14, Application US/10169223
; Publication No. US20030152946A1
; GENERAL INFORMATION:
; APPLICANT: SHIMIZU, Shigeomi
; APPLICANT: TSUJIMOTO, Yoshihide
; TITLE OF INVENTION: BH4-Fused Polypeptides
; FILE REFERENCE: 1422-0537P
; CURRENT APPLICATION NUMBER: US/10/169,223
; CURRENT FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: JP 11-371449
; PRIOR FILING DATE: 1999-12-27
; PRIOR APPLICATION NUMBER: PCT/JP00/09274
; PRIOR FILING DATE: 2000-12-26
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CDS of Synthesized DNA for mutant bcl-xL
US-10-169-223-14

```

Query Match	88.3%	Score 1075;	DB 14;	Length 212;
Best Local Similarity	97.2%;	Pred. No. 7.1e-99;		
Matches 205;	Conservative 2;	Mismatches 4;	Indels 0;	Gaps 0;
QY	23	SWQFSVDENRTEAPEETPERETPSAINGNPSWHLADSPAVNGATGCHSSSLDAREVIP	82	
DB	2	SWQFSVDENRTEAPEETPERETPSAINGNPSWHLADSPAVNGATGCHSSSLDAREVIP	61	
QY	83	MAAVKQALREAGDBFELRYRRASFDLTSQLHTPGTAYQSPQVYVNNELFRDGVNNGRIVA	142	
DB	62	MAAVKQALREAGDBFELRYRRASFDLTSQLHTPGTAYQSPQVYVNNELFRDGVNNGRIVA	121	
QY	143	FFSPGGALCVESVDKEMQVLVSRITASNMATVYLNHLPEWIOENGSGWDTFFVLYGNNAAAE	202	
DB	122	FFSPGGALCVESVDKEMQVLVSRITAMWATVYLNHLPEWIOENGSGWDTFFVLYGNNAAAE	181	
QY	203	SRKQGERFNRFWLTGMTVAGVVLGSLFSRK	233	
DB	182	SRKQGERFNRFWLTGMTVAGVVLGSLFSRK	212	

RESULT 15  
 US-10-792-517-8  
 ; Sequence 8, Application US/10792517  
 ; Publication No. US20040152179A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Youle et al.  
 ; TITLE OF INVENTION: RECEPTOR-MEDIATED UPTAKE OF AN EXTRACELLULAR BCL-XL  
 ; TITLE OF INVENTION: FUSION PROTEIN INHIBITS APOPTOSIS

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/ FILE REFERENCE: 4239-55417
/ CURRENT APPLICATION NUMBER: US/10/792,517
/ CURRENT FILING DATE: 2004-03-02
/ PRIOR APPLICATION NUMBER: US/09/639,245
/ PRIOR FILING DATE: 2000-08-15
/ PRIOR APPLICATION NUMBER: 60/149,220
/ PRIOR FILING DATE: 1999-08-16
/ NUMBER OF SEQ ID NOS: 8
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 8
/ LENGTH: 485
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: genetic fusion
US-10-792-517-8

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Query Match	87.1%	Score 1061	DB 16	Length 485
Best Local Similarity	97.1%	Pred. No. 5.6e-97		
Matches 203; Conservative	2	Mismatches 4	Indels 0	Gaps 0
QY	1	MSQSRELVDPLSYKLSQKGYSWGSFSDVEENRTEAPEETEPRETPPSAINGNPSMHLA	60	
DB	277	MSQSRELVDPLSYKLSQKGYSWGSFSDVEENRTEAPEGETSEMETPSAINGNPSMHLA	336	
QY	61	DSPAVNGATGHSSSLDAREVIPMAAQALREAGDEFELRYRRAFSDLTSLQHTTPGTAY	120	
DB	337	DSPAVNGATAHSSSLDAREVIPMAAQALREAGDEFELRYRRAFSDLTSLQHTTPGTAY	396	
QY	121	QSPSEQVNNELFRDGVNWGRIVAFPSFGGALCVESVDKEMQVLVSRIASNMWATYLNNDHLEP	180	
DB	397	QSPSEQVNNELFRDGVNWGRIVAFPSFGGALCVESVDKEMQVLVSRIAAWATYLNNDHLEP	456	
QY	181	WIOENGWDTFVDLYGNNAEAESRKGQER	209	
DB	457	WIOENGWDTFVLYGNNAEAESRKGQER	485	

Search completed: March 31, 2005, 00:34:54  
Job time : 115.019 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 31, 2005, 00:23:16 ; Search time 46.6 Seconds  
(without alignments)  
373.245 Million cell updates/sec

Title: US-10-049-822A-2  
Perfect score: 1218  
Sequence: 1 MSQSNRELVDLSYKLSQK.....FLTGMTVAGVLLGSLFSRK 233

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
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2: /cgn2\_6/ptodata/1/iaa/5B COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PTUS COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1190	97.7	233	1 US-08-333-565-59	Sequence 59, Appli
2	1190	97.7	233	1 US-08-471-058-14	Sequence 14, Appli
3	1190	97.7	233	2 US-08-661-479-59	Sequence 59, Appli
4	1190	97.7	233	3 US-08-471-057-14	Sequence 14, Appli
5	1190	97.7	233	3 US-08-481-739-2	Sequence 2, Appli
6	1190	97.7	233	4 US-08-470-865-14	Sequence 14, Appli
7	1190	97.7	233	4 US-08-155-327G-12	Sequence 12, Appli
8	1190	97.7	233	5 PCT-US94-07089-7	Sequence 7, Appli
9	1184	97.2	233	1 US-08-081-448-6	Sequence 6, Appli
10	1184	97.2	233	1 US-08-607-269-24	Sequence 24, Appli
11	1184	97.2	233	2 US-08-470-670A-7	Sequence 7, Appli
12	1184	97.2	233	3 US-08-167-921-2	Sequence 2, Appli
13	1184	97.2	233	3 US-08-323-743-2	Sequence 2, Appli
14	1184	97.2	233	3 PCT-US94-07089-7	Sequence 7, Appli
15	1184	97.2	233	5 PCT-US95-04600-24	Sequence 24, Appli
16	1184	97.2	411	4 US-09-639-245-2	Sequence 2, Appli
17	1177	96.6	233	3 US-09-271-014A-6	Sequence 6, Appli
18	1128	92.6	225	3 US-09-101-519-1	Sequence 1, Appli
19	1061	87.1	485	4 US-08-639-245-8	Sequence 8, Appli
20	979	80.4	235	4 US-08-899-367-2	Sequence 2, Appli
21	808.5	66.4	170	5 PCT-US94-07089-9	Sequence 9, Appli
22	808.5	66.4	186	4 US-09-949-016-10416	Sequence 10416, A
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24	802.5	65.9	170	2 US-08-470-670A-9	Sequence 9, Appli
25	802.5	65.9	170	3 US-08-461-511A-9	Sequence 9, Appli
26	802.5	65.9	170	3 US-09-271-014A-8	Sequence 8, Appli
27	732	60.1	190	1 US-08-081-448-2	Sequence 2, Appli

28	732	60.1	190	2 US-08-470-670A-2	Sequence 2, Appli
29	732	60.1	190	3 US-08-461-511A-2	Sequence 2, Appli
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31	732	60.1	190	5 PCT-US94-07089-2	Sequence 2, Appli
32	599	49.2	121	3 US-08-470-670A-15	Sequence 15, Appli
33	599	49.2	121	3 US-08-461-511A-15	Sequence 15, Appli
34	510	41.9	109	2 US-08-470-670A-11	Sequence 11, Appli
35	510	41.9	109	3 US-08-461-511A-11	Sequence 11, Appli
36	497	40.8	233	1 US-08-607-269-23	Sequence 23, Appli
37	497	40.8	233	5 PCT-US95-04600-23	Sequence 23, Appli
38	464	38.1	239	1 US-08-112-208C-10	Sequence 10, Appli
39	464	38.1	239	1 US-08-248-819A-10	Sequence 10, Appli
40	464	38.1	239	2 US-08-337-646A-10	Sequence 10, Appli
41	464	38.1	239	2 US-08-856-531-10	Sequence 10, Appli
42	464	38.1	239	2 US-08-856-034-10	Sequence 10, Appli
43	464	38.1	239	3 US-09-127-048-8	Sequence 8, Appli
44	464	38.1	239	3 US-08-927-326-10	Sequence 10, Appli
45	464	38.1	239	4 US-09-379-820A-10	Sequence 10, Appli

ALIGNMENTS

RESULT 1  
US-08-333-565-59  
; Sequence 59, Application US/08333565  
; Patent No. 5622852  
; GENERAL INFORMATION:  
; APPLICANT: KORSMEYER, Stanley J.  
; TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH  
; TITLE OF INVENTION: REGULATOR  
; NUMBER OF SEQUENCES: 59  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Kourie and Crew  
; STREET: 379 Lytton Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/333,565  
; FILING DATE: 31-OCT-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 15726A-000700  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 59:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 233 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-333-565-59

Query Match 97.7%; Score 1190; DB 1; Length 233;  
Best Local Similarity 97.9%; Pred. No. 5.5e-125;  
Matches 228; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 MSQSNRELVDLSYKLSQKYSWSQSDVEENRTEAPEETEPEETPSAINGNPWSHLA 60  
Db 1 MSQSNRELVDLSYKLSQKYSWSQSDVEENRTEAPEETEPEETPSAINGNPWSHLA 60  
Qy 61 DSPAVNGATGHSSSLDAREVIPMAVKAQALREAGDEFELRYRRAFSDLTSLQHTPTGAY 120



Db 61 DSPAVNGATGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHTPGTAY 120  
Qy 121 QSPFQVNNELFRDGVNNGRIVAFPSFGALCVESVDKEMQVLSRIASWMTATYLNHLEP 180  
Db 121 QSPFQVNNELFRDGVNNGRIVAFPSFGALCVESVDKEMQVLSRIASWMTATYLNHLEP 180  
Qy 181 WIQENGWDTFVDLYGNNAAESKGOERFNRWFLTGMTVAGVVLLGSLFSRK 233  
Db 181 WIQENGWDTFVELYGNNAAESKGOERFNRWFLTGMTVAGVVLLGSLFSRK 233  
RESULT 2  
US-08-471-058-14  
; Sequence 14, Application US/08471058  
; Patent No. 5770443  
; GENERAL INFORMATION:  
; APPLICANT: Kiefer, Michael C.  
; APPLICANT: Kiefer, Philip J.  
; TITLE OF INVENTION: NOVEL APOPTOSIS MODULATING  
; TITLE OF INVENTION: PROTEINS, DNA ENCODING THE PROTEINS AND METHODS OF USE  
; TITLE OF INVENTION: THEREOF  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 PAGE MILL ROAD  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/471,058  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/320,157  
; FILING DATE: 07-OCT-1994  
; APPLICATION NUMBER: 08/160,067  
; FILING DATE: 30-NOV-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lehnhardt, Susan K  
; REGISTRATION NUMBER: 33,943  
; REFERENCE/DOCKET NUMBER: 23647-20007.12  
; TELEPHONE: 415-813-5600  
; TELEFAX: 415-494-0792  
; TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 233 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-471-058-14  
Query Match 97.7%; Score 1190; DB 1; Length 233;  
Best Local Similarity 97.9%; Pred. No. 5.5e-125;  
Matches 228; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 MSQSNRELVDVFLSYKLQKGYSWSQSDVEENRTEAPEETEPEPTPSAINGNPSWHLA 60  
Db 1 MSQSNRELVDVFLSYKLQKGYSWSQSDVEENRTEAPEETEPEPTPSAINGNPSWHLA 60  
Qy 61 DSPAVNGATGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHTPGTAY 120  
Db 61 DSPAVNGATGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHTPGTAY 120  
Qy 121 QSPFQVNNELFRDGVNNGRIVAFPSFGALCVESVDKEMQVLSRIASWMTATYLNHLEP 180  
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Db 121 QSPFQVNNELFRDGVNNGRIVAFPSFGALCVESVDKEMQVLSRIASWMTATYLNHLEP 180  
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RESULT 3  
US-08-661-479-59  
; Sequence 59, Application US/08661479  
; Patent No. 5834209  
; GENERAL INFORMATION:  
; APPLICANT: KORSMEYER, Stanley J.  
; TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH  
; TITLE OF INVENTION: REGULATOR  
; NUMBER OF SEQUENCES: 59  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Kourie and Crew  
; STREET: 379 Lytton Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/661,479  
; FILING DATE: 11-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/333,565  
; FILING DATE: 31-OCT-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 15726A-000700  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 59:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 233 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-661-479-59  
Query Match 97.7%; Score 1190; DB 2; Length 233;  
Best Local Similarity 97.9%; Pred. No. 5.5e-125;  
Matches 228; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 MSQSNRELVDVFLSYKLQKGYSWSQSDVEENRTEAPEETEPEPTPSAINGNPSWHLA 60  
Db 1 MSQSNRELVDVFLSYKLQKGYSWSQSDVEENRTEAPEETEPEPTPSAINGNPSWHLA 60  
Qy 61 DSPAVNGATGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHTPGTAY 120  
Db 61 DSPAVNGATGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHTPGTAY 120  
Qy 121 QSPFQVNNELFRDGVNNGRIVAFPSFGALCVESVDKEMQVLSRIASWMTATYLNHLEP 180  
Db 121 QSPFQVNNELFRDGVNNGRIVAFPSFGALCVESVDKEMQVLSRIASWMTATYLNHLEP 180  
Qy 181 WIQENGWDTFVDLYGNNAAESKGOERFNRWFLTGMTVAGVVLLGSLFSRK 233  
Db 181 WIQENGWDTFVELYGNNAAESKGOERFNRWFLTGMTVAGVVLLGSLFSRK 233



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RESULT 4
US-08-471-057-14
; Sequence 14, Application US/08471057
; Patent No. 6015687
; GENERAL INFORMATION:
; APPLICANT: KIEFER, MICHAEL C.
; APPLICANT: BARR, PHILIP J.
; TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA
; TITLE OF INVENTION: ENCODING THE PROTEINS AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471.057
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/320,157
; FILING DATE: 07-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: LEHNHARDT, SUSAN K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 23647-20007.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-471-057-14

Query Match 97.7%; Score 1190; DB 3; Length 233;
Best Local Similarity 97.9%; Pred. No. 5.5e-125;
Matches 228; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MSQSNRELVDVFLSKYKLSQKGYSSQFSDVSENRTEAPEETEPEETPSAINGNPSWHLA 60
Db 1 MSQSNRELVDVFLSKYKLSQKGYSSQFSDVSENRTEAPEETEPEETPSAINGNPSWHLA 60
Qy 61 DSPAVNGATGHSSSLDAREVPMVAQKALREAGDEFELRYRAAFSDLTSLQHTTPGTAY 120
Db 61 DSPAVNGATGHSSSLDAREVPMVAQKALREAGDEFELRYRAAFSDLTSLQHTTPGTAY 120
Qy 121 QSPFQVNNELFRDGVNNGRIVAFPSFGALCVESVDKEMQVLVSRIASWMTYLNHLEP 180
Db 121 QSPFQVNNELFRDGVNNGRIVAFPSFGALCVESVDKEMQVLVSRIASWMTYLNHLEP 180
Qy 181 WIOENGWDHFTVDLYGNNAAESRKQGRFNRWFLTGMTVAGVVLGSLFSRK 233
Db 181 WIOENGWDHFTVDLYGNNAAESRKQGRFNRWFLTGMTVAGVVLGSLFSRK 233

RESULT 5
US-08-481-739-2
; Sequence 2, Application US/08481739
; Patent No. 6143291
; GENERAL INFORMATION:
; APPLICANT: June, Carl H. and Thompson, Craig B.
; TITLE OF INVENTION: METHODS FOR ENHANCING T CELL SURVIVAL

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; TITLE OF INVENTION: BY AUGMENTING BCL-XL PROTEIN LEVELS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/481,739
; FILING DATE: 07-JUNE-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/435,518
; FILING DATE: 04-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A. (GAD)
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: RPI-034CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-481-739-2

Query Match 97.7%; Score 1190; DB 3; Length 233;
Best Local Similarity 97.9%; Pred. No. 5.5e-125;
Matches 228; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MSQSNRELVDVFLSKYKLSQKGYSSQFSDVSENRTEAPEETEPEETPSAINGNPSWHLA 60
Db 1 MSQSNRELVDVFLSKYKLSQKGYSSQFSDVSENRTEAPEETEPEETPSAINGNPSWHLA 60
Qy 61 DSPAVNGATGHSSSLDAREVPMVAQKALREAGDEFELRYRAAFSDLTSLQHTTPGTAY 120
Db 61 DSPAVNGATGHSSSLDAREVPMVAQKALREAGDEFELRYRAAFSDLTSLQHTTPGTAY 120
Qy 121 QSPFQVNNELFRDGVNNGRIVAFPSFGALCVESVDKEMQVLVSRIASWMTYLNHLEP 180
Db 121 QSPFQVNNELFRDGVNNGRIVAFPSFGALCVESVDKEMQVLVSRIASWMTYLNHLEP 180
Qy 181 WIOENGWDHFTVDLYGNNAAESRKQGRFNRWFLTGMTVAGVVLGSLFSRK 233
Db 181 WIOENGWDHFTVDLYGNNAAESRKQGRFNRWFLTGMTVAGVVLGSLFSRK 233

RESULT 6
US-08-470-865-14
; Sequence 14, Application US/08470865
; Patent No. 6586395
; GENERAL INFORMATION:
; APPLICANT: KIEFER, MICHAEL C.
; APPLICANT: BARR, PHILIP J.
; TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA
; TITLE OF INVENTION: ENCODING THE PROTEINS AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,865
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/320,157
; FILING DATE: 07-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: LEHNHARDT, SUSAN K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 23647-20007.20
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-470-865-14

Query Match          97.7%; Score 1190; DB 4; Length 233;
Best Local Similarity 97.9%; Pred. No. 5.5e-125;
Matches 228; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MSQSNRELVDVFLSYKLSQKGSWSQFSDVEENRTEAPEETEPEETPSAINGNPSWHLA 60
Db 1 MSQSNRELVDVFLSYKLSQKGSWSQFSDVEENRTEAPEETEPEETPSAINGNPSWHLA 60

Qy 61 DSPAVNGATGHSSSLDAREVPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAY 120
Db 61 DSPAVNGATGHSSSLDAREVPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAY 120

Qy 121 OSFEQVNVNELFRDGVNNGRIVAFPSFGGALCVESVDKEMQVLVSRIASWMATYLNHLEP 180
Db 121 OSFEQVNVNELFRDGVNNGRIVAFPSFGGALCVESVDKEMQVLVSRIASWMATYLNHLEP 180

Qy 181 WIQENGWDTFVDLYGNNAEAESRKQGRFNRWFLTGMTVAGVVLGSLFSRK 233
Db 181 WIQENGWDTFVELYGNNAEAESRKQGRFNRWFLTGMTVAGVVLGSLFSRK 233

RESULT 8
PCT-US94-07089-7
; Sequence 7, Application PC/TUS9407089
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Vertebrate Apoptosis Gene:
; TITLE OF INVENTION: Compositions and Methods
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS, ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07089
; FILING DATE: CONCURRENTLY FILED
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/081.448
; FILING DATE: 22 JUNE 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: PARKER, David L.
; REGISTRATION NUMBER: 32,165
; REFERENCE/DOCKET NUMBER: ARCD090
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-320-7200
; TELEFAX: 713-789-2679
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
PCT-US94-07089-7

Query Match          97.7%; Score 1190; DB 5; Length 233;
Best Local Similarity 97.9%; Pred. No. 5.5e-125;
Matches 228; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MSQSNRELVDVFLSYKLSQKGSWSQFSDVEENRTEAPEETEPEETPSAINGNPSWHLA 60
Db 1 MSQSNRELVDVFLSYKLSQKGSWSQFSDVEENRTEAPEETEPEETPSAINGNPSWHLA 60

Qy 61 DSPAVNGATGHSSSLDAREVPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAY 120
Db 61 DSPAVNGATGHSSSLDAREVPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAY 120

Qy 121 OSFEQVNVNELFRDGVNNGRIVAFPSFGGALCVESVDKEMQVLVSRIASWMATYLNHLEP 180
Db 121 OSFEQVNVNELFRDGVNNGRIVAFPSFGGALCVESVDKEMQVLVSRIASWMATYLNHLEP 180

Query Match          97.7%; Score 1190; DB 4; Length 233;
Best Local Similarity 97.9%; Pred. No. 5.5e-125;
Matches 228; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

US-09-155-327G-12

; Sequence 12, Application US/09155327G
; Patent No. 6790637
; GENERAL INFORMATION:
; APPLICANT: AMRAD Operations Pty Ltd
; TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-2, BELONGS TO THE bcl-2
; TITLE OF INVENTION: FAMILY OF APOPTOSIS-CONTROLLING GENES
; FILE REFERENCE: 2096584
; CURRENT APPLICATION NUMBER: US/09/155,327G
; CURRENT FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: PN8965
; PRIOR FILING DATE: 1996-03-27
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Homo sapiens
;
US-09-155-327G-12

Query Match          97.7%; Score 1190; DB 4; Length 233;
Best Local Similarity 97.9%; Pred. No. 5.5e-125;
Matches 228; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
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Db 121 QSFQVNVNLPFRDGVNNGRIVAFSFGALCVESVDKEMQVLSRIAAMWATYLNHLEP 180  
 Qy 181 WIQENGGWDTFVDLYGNNAAESRKGQERFNRWFLTGMTVAGVLLGSLFSRK 233  
 Db 181 WIQENGGWDTFVDLYGNNAAESRKGQERFNRWFLTGMTVAGVLLGSLFSRK 233

RESULT 9  
 US-08-081-448-6  
 ; Sequence 6, Application US/08081448  
 ; Patent No. 5646008  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Thompson, Craig B.  
 ; APPLICANT: Boise, Lawrence H.  
 ; TITLE OF INVENTION: Vertebrate Apoptosis Gene:  
 ; TITLE OF INVENTION: Compositions and Methods  
 ; NUMBER OF SEQUENCES: 8  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Arnold, White & Durkee  
 ; STREET: 321 No. 5646008th Clark Street, Suite 800  
 ; CITY: Chicago  
 ; STATE: IL  
 ; COUNTRY: USA  
 ; ZIP: 60610  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA: US/08/081,448  
 ; APPLICATION NUMBER: 5702897  
 ; FILING DATE: 19930622  
 ; CLASSIFICATION: 424  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: No. 5646008thrup, Thomas E.  
 ; REGISTRATION NUMBER: 33,268  
 ; REFERENCE/DOCKET NUMBER: ARCD090  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 312-744-0090  
 ; TELEFAX: 312-755-4489  
 ; INFORMATION FOR SEQ ID NO: 6:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 233 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-081-448-6

Query Match 97.2%; Score 1184; DB 1; Length 233;  
 Best Local Similarity 97.4%; Pred. No. 2.6e-124;  
 Matches 227; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MSQSNRELVDFLSYKLSQKGSWSQFSDVEENTEAPEETEPEETPSAINGNPSWHLA 60  
 Db 1 MSQSNRELVDFLSYKLSQKGSWSQFSDVEENTEAPEETEPEETPSAINGNPSWHLA 60

Qy 61 DSPAVNGATGHSSSLDAREVIPMAVKQALREAGDEPELRVRRAPSDLTSLHITPGTAY 120  
 Db 61 DSPAVNGATGHSSSLDAREVIPMAVKQALREAGDEPELRVRRAPSDLTSLHITPGTAY 120

Qy 121 QSFQVNVNLPFRDGVNNGRIVAFSFGALCVESVDKEMQVLSRIAAMWATYLNHLEP 180  
 Db 121 QSFQVNVNLPFRDGVNNGRIVAFSFGALCVESVDKEMQVLSRIAAMWATYLNHLEP 180

Qy 181 WIQENGGWDTFVDLYGNNAAESRKGQERFNRWFLTGMTVAGVLLGSLFSRK 233  
 Db 181 WIQENGGWDTFVDLYGNNAAESRKGQERFNRWFLTGMTVAGVLLGSLFSRK 233

RESULT 10  
 US-08-607-269-24  
 ; Sequence 24, Application US/08607269  
 ; Patent No. 5702897

; GENERAL INFORMATION:  
 ; APPLICANT: Reed, John C.  
 ; APPLICANT: Sato, Takaaki  
 ; TITLE OF INVENTION: Interaction of Proteins Involved in a  
 ; TITLE OF INVENTION: Cell Death Pathway  
 ; NUMBER OF SEQUENCES: 29  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Campbell and Flores  
 ; STREET: 4370 La Jolla Village Drive, Suite 700  
 ; CITY: San Diego  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 92122  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA: US/08/607,269  
 ; FILING DATE:  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA: US 08/226,876  
 ; APPLICATION NUMBER: 13-APR-1994  
 ; FILING DATE: 13-APR-1994  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Campbell, Cathryn A.  
 ; REGISTRATION NUMBER: 31,815  
 ; REFERENCE/DOCKET NUMBER: P-LJ 9882  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (619) 535-9001  
 ; TELEFAX: (619) 535-8949  
 ; INFORMATION FOR SEQ ID NO: 24:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 233 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; US-08-607-269-24

Query Match 97.2%; Score 1184; DB 1; Length 233;  
 Best Local Similarity 97.4%; Pred. No. 2.6e-124;  
 Matches 227; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MSQSNRELVDFLSYKLSQKGSWSQFSDVEENTEAPEETEPEETPSAINGNPSWHLA 60  
 Db 1 MSQSNRELVDFLSYKLSQKGSWSQFSDVEENTEAPEETEPEETPSAINGNPSWHLA 60

Qy 61 DSPAVNGATGHSSSLDAREVIPMAVKQALREAGDEPELRVRRAPSDLTSLHITPGTAY 120  
 Db 61 DSPAVNGATGHSSSLDAREVIPMAVKQALREAGDEPELRVRRAPSDLTSLHITPGTAY 120

Qy 121 QSFQVNVNLPFRDGVNNGRIVAFSFGALCVESVDKEMQVLSRIAAMWATYLNHLEP 180  
 Db 121 QSFQVNVNLPFRDGVNNGRIVAFSFGALCVESVDKEMQVLSRIAAMWATYLNHLEP 180

Qy 181 WIQENGGWDTFVDLYGNNAAESRKGQERFNRWFLTGMTVAGVLLGSLFSRK 233  
 Db 181 WIQENGGWDTFVDLYGNNAAESRKGQERFNRWFLTGMTVAGVLLGSLFSRK 233

RESULT 11  
 US-08-470-670A-7  
 ; Sequence 7, Application US/08470670A  
 ; Patent No. 5834309  
 ; Patent No. 5834309 5710045  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Thompson, Craig B. B.  
 ; APPLICANT: Boise, Lawrence H.  
 ; TITLE OF INVENTION: VERTEBRATE APOPTOSIS GENE:  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS  
 ; NUMBER OF SEQUENCES: 18  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433  
 CITY: Houston  
 STATE: Texas  
 COUNTRY: United States of America  
 ZIP: 77210  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/470,670A  
 FILING DATE:  
 CLASSIFICATION: 514  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/081,448  
 FILING DATE: 22-JUN-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Highlander, Steven L.  
 REGISTRATION NUMBER: 37,642  
 REFERENCE/DOCKET NUMBER: ARCD:090--1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (512) 418-3000  
 TELEFAX: (512) 474-7577  
 INFORMATION FOR SEQ ID NO: 7:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 233 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-470-670A-7

Query Match 97.2%; Score 1184; DB 2; Length 233;  
 Best Local Similarity 97.4%; Pred. No. 2.6e-124;  
 Matches 227; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MSQSNRELVDVFLSYKLSQKGYSSQFSDVEENRTEAPEETEPEPERETPSAINGNPSWHLA 60  
 Db 1 MSQSNRELVDVFLSYKLSQKGYSSQFSDVEENRTEAPEETEPEPERETPSAINGNPSWHLA 60  
 Qy 61 DSPAVNGATGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSLQHTTPGTAY 120  
 Db 61 DSPAVNGATGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSLQHTTPGTAY 120  
 Qy 121 OSFEQVNNELFRDGVNNGRIIVAFPSFGALCVESVDKEMQVLVSRIAAWMATYLNHLEP 180  
 Db 121 OSFEQVNNELFRDGVNNGRIIVAFPSFGALCVESVDKEMQVLVSRIAAWMATYLNHLEP 180  
 Qy 181 WIQENGWDTFVDLYGNNAEAESRKQERFNRWFLTGMTVAGVVLGSLFSRK 233  
 Db 181 WIQENGWDTFVDLYGNNAEAESRKQERFNRWFLTGMTVAGVVLGSLFSRK 233

RESULT 12  
 US-09-167-921-2  
 ; Sequence 2, Application US/09167921A  
 ; Patent No. 6172216  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bennett, C. Frank  
 ; APPLICANT: Dean, Nicholas M.  
 ; APPLICANT: Monia, Brett P.  
 ; APPLICANT: Nickoloff, Brian J.  
 ; APPLICANT: Zhang, QingQing  
 ; TITLE OF INVENTION: Antisense Modulation of bcl-x Expression  
 ; FILE REFERENCE: ISPH-0324  
 ; CURRENT APPLICATION NUMBER: US/09/167,921A  
 ; CURRENT FILING DATE: 1998-10-07  
 ; NUMBER OF SEQ ID NOS: 50  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 2  
 ; LENGTH: 233  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens

US-09-167-921-2  
 Query Match 97.2%; Score 1184; DB 3; Length 233;  
 Best Local Similarity 97.4%; Pred. No. 2.6e-124;  
 Matches 227; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MSQSNRELVDVFLSYKLSQKGYSSQFSDVEENRTEAPEETEPEPERETPSAINGNPSWHLA 60  
 Db 1 MSQSNRELVDVFLSYKLSQKGYSSQFSDVEENRTEAPEETEPEPERETPSAINGNPSWHLA 60  
 Qy 61 DSPAVNGATGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSLQHTTPGTAY 120  
 Db 61 DSPAVNGATGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSLQHTTPGTAY 120  
 Qy 121 OSFEQVNNELFRDGVNNGRIIVAFPSFGALCVESVDKEMQVLVSRIAAWMATYLNHLEP 180  
 Db 121 OSFEQVNNELFRDGVNNGRIIVAFPSFGALCVESVDKEMQVLVSRIAAWMATYLNHLEP 180  
 Qy 181 WIQENGWDTFVDLYGNNAEAESRKQERFNRWFLTGMTVAGVVLGSLFSRK 233  
 Db 181 WIQENGWDTFVDLYGNNAEAESRKQERFNRWFLTGMTVAGVVLGSLFSRK 233

RESULT 13  
 US-09-323-743-2  
 ; Sequence 2, Application US/09323743  
 ; Patent No. 6214986  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bennett, C. Frank  
 ; APPLICANT: Dean, Nicholas M.  
 ; APPLICANT: Monia, Brett P.  
 ; APPLICANT: Nickoloff, Brian J.  
 ; APPLICANT: Zhang, QingQing  
 ; TITLE OF INVENTION: Antisense Modulation of bcl-x Expression  
 ; FILE REFERENCE: ISPH-0368  
 ; CURRENT APPLICATION NUMBER: US/09/323,743  
 ; CURRENT FILING DATE: 1999-06-01  
 ; EARLIER APPLICATION NUMBER: 09/277,020  
 ; EARLIER FILING DATE: 1998-03-26  
 ; EARLIER APPLICATION NUMBER: 09/167,921  
 ; EARLIER FILING DATE: 1998-10-07  
 ; NUMBER OF SEQ ID NOS: 66  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 2  
 ; LENGTH: 233  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens

US-09-323-743-2  
 Query Match 97.2%; Score 1184; DB 3; Length 233;  
 Best Local Similarity 97.4%; Pred. No. 2.6e-124;  
 Matches 227; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MSQSNRELVDVFLSYKLSQKGYSSQFSDVEENRTEAPEETEPEPERETPSAINGNPSWHLA 60  
 Db 1 MSQSNRELVDVFLSYKLSQKGYSSQFSDVEENRTEAPEETEPEPERETPSAINGNPSWHLA 60  
 Qy 61 DSPAVNGATGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSLQHTTPGTAY 120  
 Db 61 DSPAVNGATGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSLQHTTPGTAY 120  
 Qy 121 OSFEQVNNELFRDGVNNGRIIVAFPSFGALCVESVDKEMQVLVSRIAAWMATYLNHLEP 180  
 Db 121 OSFEQVNNELFRDGVNNGRIIVAFPSFGALCVESVDKEMQVLVSRIAAWMATYLNHLEP 180  
 Qy 181 WIQENGWDTFVDLYGNNAEAESRKQERFNRWFLTGMTVAGVVLGSLFSRK 233  
 Db 181 WIQENGWDTFVDLYGNNAEAESRKQERFNRWFLTGMTVAGVVLGSLFSRK 233

RESULT 14  
 US-08-461-511A-7  
 ; Sequence 7, Application US/08461511A

Patent No. 6303331  
GENERAL INFORMATION:  
APPLICANT: Thompson, Craig B.B.  
Boise, Lawrence H.  
TITLE OF INVENTION: VERTEBRATE APOPTOSIS GENE: COMPOSITIONS  
AND METHODS  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: United States of America  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/461,511A  
FILING DATE: 05-Jun-1995  
CLASSIFICATION: UNKNOWN  
ATTORNEY/AGENT INFORMATION:  
NAME: Highlander, Steven L.  
REGISTRATION NUMBER: 37,642  
REFERENCE/DOCKET NUMBER: ARCD:179  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (512) 418-3000  
TELEFAX: (512) 474-7577  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 233 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
US-08-461-511A-7  
Query Match 97.2%; Score 1184; DB 3; Length 233;  
Best Local Similarity 97.4%; Pred. No. 2.6e-124;  
Matches 227; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
Qy 1 MSQSNRELVDVFLSYKLSQKGYNSQFSQSDVEENRTEAPEETEPEPTPSAINGNPSWHLA 60  
Db 1 MSQSNRELVDVFLSYKLSQKGYNSQFSQSDVEENRTEAPEETEPEPTPSAINGNPSWHLA 60  
Qy 61 DSPAVNGATGHSSSLDAREVPMMAVKQALREAGDEPELRYRRRAFSDLTSQLHTPGTAY 120  
Db 61 DSPAVNGATGHSSSLDAREVPMMAVKQALREAGDEPELRYRRRAFSDLTSQLHTPGTAY 120  
Qy 121 QSFQVNVNELFRDGVNMGRIVAFFSFGALCVESVDKEMQVLVSRIASWMATYLNHLEP 180  
Db 121 QSFQVNVNELFRDGVNMGRIVAFFSFGALCVESVDKEMQVLVSRIASWMATYLNHLEP 180  
Qy 181 WIQENGWDTFVDLYGNNAAESRKQERFNRWFLTGMTVAGVLLGSLFSRK 233  
Db 181 WIQENGWDTFVDLYGNNAAESRKQERFNRWFLTGMTVAGVLLGSLFSRK 233

RESULT 15  
PCT-US95-04600-24  
Sequence 24, Application PC/TUS9504600  
GENERAL INFORMATION:  
APPLICANT: LA JOLLA CANCER RESEARCH FOUNDATION  
TITLE OF INVENTION: Interaction of Proteins Involved in  
NUMBER OF SEQUENCES: a Cell Death Pathway  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Campbell and Flores  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California

COUNTRY: USA  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/04600  
FILING DATE: 12-APR-1995  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Imbra, Richard J.  
REGISTRATION NUMBER: 37,643  
REFERENCE/DOCKET NUMBER: PP-LJ 1361  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 233 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
PCT-US95-04600-24  
Query Match 97.2%; Score 1184; DB 5; Length 233;  
Best Local Similarity 97.4%; Pred. No. 2.6e-124;  
Matches 227; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
Qy 1 MSQSNRELVDVFLSYKLSQKGYNSQFSQSDVEENRTEAPEETEPEPTPSAINGNPSWHLA 60  
Db 1 MSQSNRELVDVFLSYKLSQKGYNSQFSQSDVEENRTEAPEETEPEPTPSAINGNPSWHLA 60  
Qy 61 DSPAVNGATGHSSSLDAREVPMMAVKQALREAGDEPELRYRRRAFSDLTSQLHTPGTAY 120  
Db 61 DSPAVNGATGHSSSLDAREVPMMAVKQALREAGDEPELRYRRRAFSDLTSQLHTPGTAY 120  
Qy 121 QSFQVNVNELFRDGVNMGRIVAFFSFGALCVESVDKEMQVLVSRIASWMATYLNHLEP 180  
Db 121 QSFQVNVNELFRDGVNMGRIVAFFSFGALCVESVDKEMQVLVSRIASWMATYLNHLEP 180  
Qy 181 WIQENGWDTFVDLYGNNAAESRKQERFNRWFLTGMTVAGVLLGSLFSRK 233  
Db 181 WIQENGWDTFVDLYGNNAAESRKQERFNRWFLTGMTVAGVLLGSLFSRK 233  
Search completed: March 31, 2005, 00:32:37  
Job time : 48.6 secs

Handwritten text, possibly a signature or a small note, oriented vertically.

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 31, 2005, 00:17:06 ; Search time 163.1 Seconds  
(without alignments)  
552.515 Million cell updates/sec

Title: US-10-049-822a-2  
Perfect score: 1218  
Sequence: 1 MSQSNRELVDVFLSYKLSQK.....FLGTMTVAGVLLGSLFSRK 233

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

- 1: Geneseq1980s:\*
- 2: Geneseq1990s:\*
- 3: Geneseq2000s:\*
- 4: Geneseq2001s:\*
- 5: Geneseq2002s:\*
- 6: Geneseq2003as:\*
- 7: Geneseq2003bs:\*
- 8: Geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
1	1218	100.0	233	4	AAB73303 Rat wild-
2	1218	100.0	233	7	AD622921 Rat Prote
3	1218	100.0	233	7	AD62491 Rat Prote
4	1210	99.3	233	8	ADQ80678 Mouse ant
5	1206	99.0	233	4	AAB73304 Mutant ra
6	1197	98.3	237	5	ABG78480 Wild type
7	1196	98.2	233	8	ADH52633 Chinese h
8	1190	97.7	233	2	AA68887 Human thy
9	1190	97.7	233	2	AAW05821 Bcl-XL pr
10	1190	97.7	233	2	AAW31530 Human ant
11	1190	97.7	233	7	AD62493 Human Pro
12	1190	97.7	233	8	ADM45995 Human apo
13	1190	97.7	233	8	ADM04261 Antipsori
14	1190	97.7	233	8	ADO19867 Human PRO
15	1190	97.7	233	8	ABM82217 Tumour-as
16	1190	97.7	233	8	ADP54629 Human PRO
17	1190	97.7	233	8	ADP54992 Human PRO
18	1190	97.7	233	8	ADP24510 PRO poly
19	1190	97.7	233	8	ADP23990 PRO poly
20	1190	97.7	249	8	ADQ97766 Human can
21	1187	97.5	233	8	ADQ80677 Human ant
22	1184	97.2	233	3	AA69969 Human Bcl
23	1184	97.2	233	3	AA83223 Bcl-x pol
24	1184	97.2	233	4	AAB50538 Human Bcl
25	1184	97.2	233	4	AAG64262 Human Bcl

26	1184	97.2	233	4	AAB47515	Aab47515 Protein e
27	1184	97.2	233	7	ABW02410	ABW02410 Human bcl
28	1184	97.2	233	8	ADO19991	ADO19991 Human PRO
29	1184	97.2	233	8	ADQ80670	ADQ80670 Human ant
30	1184	97.2	411	4	AAU00219	AAU00219 Bcl-XL-DT
31	1182	97.0	342	8	ADQ97763	ADQ97763 Mouse can
32	1181	97.0	233	8	ADQ80679	ADQ80679 Porcine a
33	1179	96.8	236	6	ABR83558	ABR83558 ToJA-BCL
34	1179	96.8	348	6	ABR83557	ABR83557 ToJA-BCL
35	1146.5	94.1	230	7	ADF60832	ADF60832 Human Bcl
36	1128	92.6	225	2	AAW19396	AAW19396 "Deprenyl
37	1090	89.5	219	8	ADH52639	ADH52639 Chinese h
38	1079	88.6	219	8	ADH52641	ADH52641 Chinese h
39	1078	88.5	212	4	AAB20495	AAB20495 Human Bcl
40	1078	88.5	212	8	ADG65210	ADG65210 Human Bcl
41	1075	88.3	212	4	AAG64285	AAG64285 Mutant bc
42	1061	87.1	485	4	AAU00222	AAU00222 LFn-Bcl-X
43	987.5	81.1	229	5	AAO18222	AAO18222 Human Bcl
44	975	80.4	235	2	AAW48312	AAW48312 Mouse BCL
45	967	79.4	199	8	ADH52637	ADH52637 Chinese h

## ALIGNMENTS

### RESULT 1

AAB73303  
ID AAB73303 standard; protein; 233 AA.

XX AAB73303;

AC AAB73303;

XX 22-MAY-2001 (first entry)

DT Rat wild-type Bcl-XL protein.

XX Rat Bcl-XL; apoptosis inhibitor; programmed cell death inhibitor;

XX wild-type; antiapoptotic; cell death-associated disease;

XX tissue transplant preservative.

OS Rattus norvegicus.

XX WO200112807-A1.

XX 22-FEB-2001.

XX 17-AUG-2000; 2000WO-JP005502.

XX 17-AUG-1999; 99JP-00230642.

XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.

XX Ohta S, Asoh S;

XX WPI; 2001-211219/21.

XX N-ESDB; AAF75960.

XX Modified cDNA of rat bcl-x gene and encoded protein with membrane

XX permeability to enhance uptake for effective inhibition of cell death

XX e.g. apoptosis, useful in remedies for diseases associated with cell

XX death.

XX Claim 6; Page 45-46; 56pp; Japanese.

XX The invention relates to a mutant rat Bcl-x protein and the cDNA encoding

XX it. The mutant rat Bcl-x protein (Bcl-xFNK) has the substitutions Y22F,

XX Q26N, and R165K relative to the wild-type Bcl-XL protein. The invention

XX also encompasses recombinant vectors and host cells comprising the

XX modified nucleic acid sequence. The mutant Bcl-x protein is able to

XX permeate the cell membrane, thus enhancing its ability to be taken up

XX into a cell and to act as an inhibitor of apoptosis (programmed cell

XX death). Bcl-xFNK and nucleic acids encoding it are useful in remedies for

XX diseases associated with cell death and in additives for maintaining the

XX stability of transplanted cells and organs. The present sequence

```
CC represents wild-type rat Bcl-xL
XX
SQ Sequence 233 AA;

Query Match      100.0%; Score 1218; DB 4; Length 233;
Best Local Similarity 100.0%; Pred. No. 5.8e-121;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSQSNRELVDVFLSYKLSQKGYSWQSDVEENTEAPEETEPRETPSAINGNPWSHLA 60
Dy 1 MSQSNRELVDVFLSYKLSQKGYSWQSDVEENTEAPEETEPRETPSAINGNPWSHLA 60
Qy 61 DSPAVNGATGHSSSLDAREVPMAAVKQALREAGDEFELRYRRAFSDLTSQLHTTPGTAY 120
Dy 61 DSPAVNGATGHSSSLDAREVPMAAVKQALREAGDEFELRYRRAFSDLTSQLHTTPGTAY 120
Qy 121 QSFEQVNNELFRDGVNNGRIVAFPSFGGALCVESVDKEMQVLVSRIASWMTATYLNHLEP 180
Dy 121 QSFEQVNNELFRDGVNNGRIVAFPSFGGALCVESVDKEMQVLVSRIASWMTATYLNHLEP 180
Qy 181 WIQENGWDTFVDLYGNNAASERKQGRFNRWFLTGMTVAGVVLGSLFSRK 233
Dy 181 WIQENGWDTFVDLYGNNAASERKQGRFNRWFLTGMTVAGVVLGSLFSRK 233

RESULT 2
ADE62921
ID ADE62921 standard; protein; 233 AA.
AC ADE62921;
XX
XX 29-JAN-2004 (first entry)
DT
DE Rat Protein P53563, SEQ ID NO 8855.
KW Rat; pain; neuronal tissue; Gene therapy; spinal segmental nerve injury;
XX chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX Rattus norvegicus.
OS
XX WO2003016475-A2.
XX
XX 27-FEB-2003.
XX
XX 14-AUG-2002; 2002WO-US025765.
XX
XX 14-AUG-2001; 2001US-0312147P.
XX 01-NOV-2001; 2001US-0346382P.
XX 26-NOV-2001; 2001US-0333347P.
XX
XX (GEHO ) GEN HOSPITAL CORP.
XX
XX Woolf C, D'urso D, Befort K, Costigan M;
XX
XX WPI; 2003-268312/26.
XX
XX GENBANK; P53563.
XX
XX New composition comprising two or more isolated polypeptides, useful for
XX preparing a medicament for treating pain in an animal.
XX
XX Claim 1; Page; 1017pp; English.
XX
XX The invention discloses a composition comprising two or more isolated rat
XX or human polynucleotides or a polynucleotide which represents a fragment,
XX derivative or allelic variation of the nucleic acid sequence. Also
XX claimed are a vector comprising the novel polynucleotide, a host cell
XX comprising the vector, a method for identifying a nucleotide sequence
XX which is differentially regulated in an animal subjected to pain and a
XX kit to perform the method, an array, a method for identifying an agent
XX that increases or decreases the expression of the polynucleotide sequence
XX that is differentially expressed in neuronal tissue of a first animal
XX subjected to pain, a method for identifying a compound which regulates
```

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CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. Gene
CC therapy). The sequence presented is a rat protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 233 AA;

Query Match      100.0%; Score 1218; DB 7; Length 233;
Best Local Similarity 100.0%; Pred. No. 5.8e-121;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSQSNRELVDVFLSYKLSQKGYSWQSDVEENTEAPEETEPRETPSAINGNPWSHLA 60
Dy 1 MSQSNRELVDVFLSYKLSQKGYSWQSDVEENTEAPEETEPRETPSAINGNPWSHLA 60
Qy 61 DSPAVNGATGHSSSLDAREVPMAAVKQALREAGDEFELRYRRAFSDLTSQLHTTPGTAY 120
Dy 61 DSPAVNGATGHSSSLDAREVPMAAVKQALREAGDEFELRYRRAFSDLTSQLHTTPGTAY 120
Qy 121 QSFEQVNNELFRDGVNNGRIVAFPSFGGALCVESVDKEMQVLVSRIASWMTATYLNHLEP 180
Dy 121 QSFEQVNNELFRDGVNNGRIVAFPSFGGALCVESVDKEMQVLVSRIASWMTATYLNHLEP 180
Qy 181 WIQENGWDTFVDLYGNNAASERKQGRFNRWFLTGMTVAGVVLGSLFSRK 233
Dy 181 WIQENGWDTFVDLYGNNAASERKQGRFNRWFLTGMTVAGVVLGSLFSRK 233

RESULT 3
ADE62491
ID ADE62491 standard; protein; 233 AA.
XX
XX ADE62491;
XX
XX 29-JAN-2004 (first entry)
DT
XX Rat Protein P53563, SEQ ID NO 8420.
DE
XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
XX chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX Rattus norvegicus.
OS
XX WO2003016475-A2.
XX
XX 27-FEB-2003.
XX
XX 14-AUG-2002; 2002WO-US025765.
XX
XX 14-AUG-2001; 2001US-0312147P.
XX 01-NOV-2001; 2001US-0346382P.
XX 26-NOV-2001; 2001US-0333347P.
XX
XX (GEHO ) GEN HOSPITAL CORP.
XX (FARB ) BAYER AG.
XX
XX Woolf C, D'urso D, Befort K, Costigan M;
XX
XX WPI; 2003-268312/26.
XX
XX GENBANK; P53563.
XX
```



XX New composition comprising two or more isolated polypeptides, useful for  
PT preparing a medicament for treating pain in an animal.  
XX  
XX  
XX Claim 1; Page; 1017pp; English.  
XX  
XX The invention discloses a composition comprising two or more isolated rat  
CC or human polynucleotides or a polynucleotide which represents a fragment,  
CC derivative or allelic variation of the nucleic acid sequence. Also  
CC claimed are a vector comprising the novel polynucleotide, a host cell  
CC comprising the vector, a method for identifying a nucleotide sequence  
CC which is differentially regulated in an animal subjected to pain and a  
CC kit to perform the method, an array, a method for identifying an agent  
CC that increases or decreases the expression of the polynucleotide sequence  
CC that is differentially expressed in neuronal tissue of a first animal  
CC subjected to pain, a method for identifying a compound which regulates  
CC the expression of a polynucleotide sequence which is differentially  
CC expressed in an animal subjected to pain, a method for identifying a  
CC compound that regulates the activity of one or more of the  
CC polynucleotides, a method for producing a pharmaceutical composition, a  
CC method for identifying a compound or small molecule that regulates the  
CC activity in an animal of one or more of the polypeptides given in the  
CC specification, a method for identifying a compound useful in treating  
CC pain and a pharmaceutical composition comprising the one or more  
CC polypeptides or their antibodies. The polynucleotide or the compound that  
CC modulates its activity is useful for preparing a medicament for treating  
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
CC therapy). The sequence presented is a rat protein (shown in Table 2 of  
CC the specification) which is differentially expressed during pain. Note:  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic form directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
XX SQ Sequence 233 AA;

Query Match 100.0%; Score 1218; DB 7; Length 233;  
Best Local Similarity 100.0%; Pred. No. 5.8e-121;  
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MSQSNRELVDVFLSYKLSQKGSWSQSDVEENRTEAPEETEPRETPSAINGNPSWHLA 60  
Db 1 MSQSNRELVDVFLSYKLSQKGSWSQSDVEENRTEAPEETEPRETPSAINGNPSWHLA 60  
Qy 61 DSPAVNGATGHSLSLDAREVTPMAAVKQALREAGDEFEELRYRRFSDLTSLHTPTGAY 120  
Db 61 DSPAVNGATGHSLSLDAREVTPMAAVKQALREAGDEFEELRYRRFSDLTSLHTPTGAY 120  
Qy 121 QSPFQVNNELFRDGVNNGRIVAFPSFGALCVESVDKEMQVLSRIASWATYLNHLEP 180  
Db 121 QSPFQVNNELFRDGVNNGRIVAFPSFGALCVESVDKEMQVLSRIASWATYLNHLEP 180  
Qy 181 WIQENGWDTFVDLYGNNAAESRKGQERFNRWLTGTVAGVVLGSLPSRK 233  
Db 181 WIQENGWDTFVDLYGNNAAESRKGQERFNRWLTGTVAGVVLGSLPSRK 233

RESULT 4  
ADQ80678  
ID ADQ80678 standard; protein; 233 AA.  
XX  
XX AC ADQ80678;  
XX  
XX DT 21-OCT-2004 (first entry)  
XX  
XX DE Mouse anti-apoptotic Bcl-XL protein.  
XX  
XX KW Survival; neuron; tyrosine hydroxylase; tyrosine 3-monooxygenase; TH;  
KW anti-apoptotic; Bcl-XL; neurological disorder; neuroprotective;  
KW norepinephrine; antiparkinsonian; transplantation; drug screening;  
KW gene profiling; CNS disorder; neurodegenerative disease; mouse; murine.  
XX  
XX OS Mus musculus.

XX WO2004062554-A2.  
XX  
XX PD 29-JUL-2004.  
XX  
XX PF 07-JAN-2004; 2004WO-DK000008.  
XX  
XX PR 08-JAN-2003; 2003US-0438719P.  
XX  
XX PR 11-APR-2003; 2003DK-00000581.  
XX  
XX PR 22-APR-2003; 2003US-0464546P.  
XX  
XX PA (NSGE-) NSGENE AS.  
XX  
XX PI Martinez-Serrano A, Liste I, Villa A;  
XX WPI; 2004-544027/52.  
XX  
XX PT Enhancing the survival of neurons or cells expressing tyrosine  
PT hydroxylase (TH) for treating neurodegenerative disorders, comprises  
PT contacting neurons or TH expressing cells with Bcl-XL or its functional  
PT equivalent.  
XX  
XX PS Claim 21; SEQ ID NO 9; 108pp; English.  
XX  
XX CC The invention relates to a novel method for enhancing the survival of  
CC neurons and/or of cells expressing tyrosine hydroxylase (EC 1.14.16.2 -  
CC Tyrosine 3-monooxygenase) (TH + ). The method comprises contacting a  
CC population of cells with Bcl-XL or its functional equivalent, where the  
CC population of cells is selected from: neurons or cells capable of  
CC differentiating into neurons; or TH expressing cells or cells capable of  
CC differentiating into TH expressing cells. The invention further  
CC comprises: a composition of cells obtainable by the method above; a  
CC composition of isolated mammalian cells overexpressing the anti-apoptotic  
CC Bcl-XL protein; a neural progenitor cell; a differentiated dopaminergic  
CC neuron; an implantable cell culture device comprising: a semi-permeable  
CC membrane permitting the diffusion of a biologically active protein  
CC through it; and a composition of cells selected from above; a lentiviral  
CC vector particle being produced based on a lentiviral transfer vector;  
CC enhancing the survival of TH + cells in vivo; a retroviral particle being  
CC produced based on a retroviral transfer vector; enhancing the survival of  
CC in vivo differentiated dopaminergic neurons; a packaging cell line  
CC capable of producing an infective vector particle; a packaging cell line  
CC capable of producing an infective vector particle; treatment of a  
CC neurological disorder; a fusion protein comprising the Bcl-XL sequence  
CC comprising 233 amino acids ADQ80670 or its functional equivalent and a  
CC membrane translocation signal; an expression vector comprising a  
CC polynucleotide sequence coding for the fusion protein and a promoter  
CC sequence capable of directing the expression of the fusion protein in a  
CC host cell; a host cell comprising the expression vector; and producing  
CC the fusion protein. The compositions of the invention have  
CC neuroprotective, neurotropic, and antiparkinsonian activities. The cells  
CC are useful for transplantation, drug screening, gene profiling, or for  
CC the preparation of a medicament useful for the treatment of a CNS  
CC disorder. The CNS disorder is a neurodegenerative disease involving  
CC neurons and traumatic neurons, including traumatic lesions of peripheral  
CC nerves, the medulla, the spinal cord, cerebral ischaemic neuronal  
CC damage, neuropathy, peripheral neuropathy, Alzheimer's disease,  
CC Huntington's disease, Parkinson's disease, amyotrophic lateral sclerosis,  
CC or memory impairment connected to dementia. The method is useful for  
CC enhancing the survival of neurons and/or of cells expressing tyrosine  
CC hydroxylase for the treatment of neurodegenerative disorders. This  
CC sequence represents a mouse anti-apoptotic Bcl-XL protein, used in the  
CC method for increasing the survival rate of neurons of the invention.  
XX  
XX SQ Sequence 233 AA;

Query Match 99.3%; Score 1210; DB 8; Length 233;  
Best Local Similarity 99.6%; Pred. No. 4.1e-120;  
Matches 232; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 MSQSNRELVDVFLSYKLSQKGSWSQSDVEENRTEAPEETEPRETPSAINGNPSWHLA 60  
Db 1 MSQSNRELVDVFLSYKLSQKGSWSQSDVEENRTEAPEETEPRETPSAINGNPSWHLA 60

Qy 61 DSPAVNGATGHSSSLDAREVPMMAVKQALREAGDEPELRYRRRAFSDLTSLQHTTPTGAY 120  
 Db 61 DSPAVNGATGHSSSLDAREVPMMAVKQALREAGDEPELRYRRRAFSDLTSLQHTTPTGAY 120  
 Qy 121 QSFEQVVNELFRDGVNMGRIIVAFSFGGALCVESVDKEMQVLVSRIASWMATYLNHLEP 180  
 Db 121 QSFEQVVNELFRDGVNMGRIIVAFSFGGALCVESVDKEMQVLVSRIASWMATYLNHLEP 180  
 Qy 181 WIOENGWDTFTVDLYGNNAASERKGOERFNRWFLTGMTVAGVVLGSLFSRK 233  
 Db 181 WIOENGWDTFTVDLYGNNAASERKGOERFNRWFLTGMTVAGVVLGSLFSRK 233

RESULT 5  
 AAB73304  
 ID AAB73304 standard; protein; 233 AA.  
 AC AAB73304;  
 XX  
 DT 22-MAY-2001 (first entry)  
 XX  
 DE Mutant rat Bcl-xL protein, Bcl-xFNK.  
 XX  
 KW Rat Bcl-xL mutant; Bcl-xFNK; apoptosis inhibitor; membrane permeable;  
 KW programmed cell death inhibitor; wild-type; antiapoptotic;  
 KW cell death-associated disease; tissue transplant preservative; mutein.  
 XX  
 OS Rattus norvegicus.  
 OS Synthetic.  
 XX  
 PN WO200112807-A1.  
 XX  
 PD 22-FEB-2001.  
 XX  
 PF 17-AUG-2000; 2000WO-JP005502.  
 XX  
 PR 17-AUG-1999; 99JP-00230642.  
 XX  
 PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.  
 XX  
 PI Ohta S, Asoh S;  
 XX  
 WPI; 2001-211219/21.  
 XX

Modified cDNA of rat bcl-x gene and encoded protein with membrane permeability to enhance uptake for effective inhibition of cell death e.g. apoptosis, useful in remedies for diseases associated with cell death.  
 Claim 1; Page 46-47; 56pp; Japanese.  
 The invention relates to a mutant rat Bcl-x protein and the cDNA encoding it. The mutant rat Bcl-x protein (Bcl-xFNK) has the substitutions Y22F, Q26N, and R165K relative to the wild-type Bcl-xL protein. The invention also encompasses recombinant vectors and host cells comprising the modified nucleic acid sequence. The mutant Bcl-x protein is able to permeate the cell membrane, thus enhancing its ability to be taken up into a cell and to act as an inhibitor of apoptosis (programmed cell death). Bcl-xFNK and nucleic acids encoding it are useful in remedies for diseases associated with cell death and in additives for maintaining the stability of transplanted cells and organs. The present sequence represents the mutant rat Bcl-xL protein, Bcl-xFNK  
 Query Match 99.0%; Score 1206; DB 4; Length 233;  
 Best Local Similarity 98.7%; Pred. No. 1.1e-119;  
 Matches 230; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 Sequence 233 AA;  
 Qy 1 MSQSNRELVDVFLSYKLSQKGYSMQSDVEENRTEAPEETEPEETPSAINGNPSWHLA 60  
 Db 1 MSQSNRELVDVFLSYKLSQKGYSMQSDVEENRTEAPEETEPEETPSAINGNPSWHLA 60

Qy 61 DSPAVNGATGHSSSLDAREVPMMAVKQALREAGDEPELRYRRRAFSDLTSLQHTTPTGAY 120  
 Db 61 DSPAVNGATGHSSSLDAREVPMMAVKQALREAGDEPELRYRRRAFSDLTSLQHTTPTGAY 120  
 Qy 121 QSFEQVVNELFRDGVNMGRIIVAFSFGGALCVESVDKEMQVLVSRIASWMATYLNHLEP 180  
 Db 121 QSFEQVVNELFRDGVNMGRIIVAFSFGGALCVESVDKEMQVLVSRIASWMATYLNHLEP 180  
 Qy 181 WIOENGWDTFTVDLYGNNAASERKGOERFNRWFLTGMTVAGVVLGSLFSRK 233  
 Db 181 WIOENGWDTFTVDLYGNNAASERKGOERFNRWFLTGMTVAGVVLGSLFSRK 233

RESULT 6  
 ABG78480  
 ID ABG78480 standard; protein; 237 AA.  
 AC ABG78480;  
 XX  
 DT 15-NOV-2002 (first entry)  
 XX  
 DE Wild type BclX1 protein.  
 XX  
 KW Human; Bcl2; BclX1; programmed cell death; apoptosis; mutant; mutein.  
 XX  
 OS Homo sapiens.  
 OS WO200240530-A2.  
 XX  
 PN 23-MAY-2002.  
 XX  
 PD 15-NOV-2001; 2001WO-US045693.  
 XX  
 PF 20-NOV-2000; 2000US-00716395.  
 XX  
 PR (ABBO ) ABBOTT LAB.  
 XX  
 PA Pesik SW, Petros AM, Yoon H, Nettesheim DG;  
 XX  
 WPI; 2002-490141/52.  
 XX

New mutant Bcl-2 proteins derived from a wild type human Bcl-2 protein, useful in biological assays to identify substances that block the ability of Bcl-2 to inhibit programmed cell death or apoptosis.  
 Disclosure; Fig 1; 36pp; English.  
 This invention relates to a novel mutant protein which is derived from a wild type human Bcl-2 protein. The mutant is created by replacing a sequence of amino acid residues comprising a flexible loop from the wild type Bcl-2 protein with an amino acid sequence comprising at least two acidic amino acids. The mutant Bcl-2 protein comprises a 166 residue shown in the specification. The invention also comprises an assay for identifying substances that bind to the Bcl-2 protein. The protein sequences of the invention are useful in biological assays to identify substances that block the ability of Bcl-2 to inhibit programmed cell death or apoptosis. The present sequence represents a human Bcl2 mutant protein used in the invention  
 Query Match 98.3%; Score 1197; DB 5; Length 237;  
 Best Local Similarity 98.3%; Pred. No. 1e-118;  
 Matches 229; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 Sequence 237 AA;  
 Qy 1 MSQSNRELVDVFLSYKLSQKGYSMQSDVEENRTEAPEETEPEETPSAINGNPSWHLA 60  
 Db 5 MSQSNRELVDVFLSYKLSQKGYSMQSDVEENRTEAPEETEPEETPSAINGNPSWHLA 64  
 Qy 61 DSPAVNGATGHSSSLDAREVPMMAVKQALREAGDEPELRYRRRAFSDLTSLQHTTPTGAY 120  
 Db 65 DSPAVNGATGHSSSLDAREVPMMAVKQALREAGDEPELRYRRRAFSDLTSLQHTTPTGAY 124

QY 121 QSEFQVNNELFRDGVNNGRIVAFPSFGALCVESVDKEMQVLSRIASWMMATYLNHLEP 180  
DB 125 QSEFQVNNELFRDGVNNGRIVAFPSFGALCVESVDKEMQVLSRIASWMMATYLNHLEP 184

QY 181 WIQENGWDTFVDLYGNNAASRKQGERFNRWFLTGMTVAGVVLLGSLFSRK 233  
DB 185 WIQENGWDTFVELYGNNAASRKQGERFNRWFLTGMTVAGVVLLGSLFSRK 237

RESULT 7  
ADH52633  
ID ADH52633 standard; protein; 233 AA.  
XX AC ADH52633;  
XX 25-MAR-2004 (first entry)  
XX Chinese hamster anti-apoptosis bcl-xL wild-type protein.  
XX mammalian myeloma host cell; protein production; anti-apoptosis;  
XX cell death; Chinese hamster; bcl-xL; wild-type.  
XX Cricetulus griseus.  
XX US2003219871-A1.  
XX 27-NOV-2003.  
XX 28-MAR-2003; 2003US-00402017.  
XX 02-APR-2002; 2002US-0369307P.  
XX (BOEH ) BOEHRINGER INGELHEIM PHARMA GMBH & CO KG.  
XX Enekel B, Meents H, Fussenegger M;  
XX WPI; 2004-033642/03.  
XX N-PSDB; ADH52632.  
XX New genetically engineered hamster or murine myeloma host cells  
PT comprising enhanced levels of active anti-apoptosis genes, useful for  
PT producing complex protein therapeutics.  
XX Disclosure; SEQ ID NO 4; 46pp; English.

CC The invention relates to a novel mammalian host cell for producing  
CC protein therapeutics. The host cell comprises a hamster or a murine  
CC myeloma cell that is genetically modified by introduction of nucleic acid  
CC sequences encoding an anti-apoptosis gene, a selectable amplifiable  
CC marker gene and at least one gene of interest. The host cell of the  
CC invention may be useful for producing at least one protein encoded by a  
CC gene of interest. The DNA, polypeptide and the methods may be used for  
CC inhibiting or delaying cell death. The current sequence is that of the  
CC Chinese hamster anti-apoptosis bcl-xL wild-type protein of the invention.

XX Sequence 233 AA;  
SQ

Query Match 98.2%; Score 1196; DB 8; Length 233;  
Best Local Similarity 98.3%; Pred. No. 1.3e-118;  
Matches 229; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSQSNRELVDVFLSYKLSQKGYSSQSDVEENRTEAPEETPERETPSAINGNPSWHLA 60  
DB 1 MSQSNRELVDVFLSYKLSQKGYSSQSDVEENRTEAPEETPERETPSAINGNPSWHLA 60

QY 61 DSPAVNGATGHSSSLDAREVIPAQAALREAGDEFEFLRYRRFSDLTSLHITPGTAY 120  
DB 61 DSPAVNGATGHSSSLDAREVIPAQAALREAGDEFEFLRYRRFSDLTSLHITPGTAY 120

QY 121 QSEFQVNNELFRDGVNNGRIVAFPSFGALCVESVDKEMQVLSRIASWMMATYLNHLEP 180  
DB 121 QSEFQVNNELFRDGVNNGRIVAFPSFGALCVESVDKEMQVLSRIASWMMATYLNHLEP 180

QY 121 QSEFQVNNELFRDGVNNGRIVAFPSFGALCVESVDKEMQVLSRIASWMMATYLNHLEP 180  
DB 121 QSEFQVNNELFRDGVNNGRIVAFPSFGALCVESVDKEMQVLSRIASWMMATYLNHLEP 180

QY 181 WIQENGWDTFVDLYGNNAASRKQGERFNRWFLTGMTVAGVVLLGSLFSRK 233  
DB 181 WIQENGWDTFVELYGNNAASRKQGERFNRWFLTGMTVAGVVLLGSLFSRK 233

RESULT 8  
AAR68887  
ID AAR68887 standard; protein; 233 AA.  
XX AC AAR68887;  
XX 25-MAR-2003 (revised)  
DT 10-AUG-1995 (first entry)  
XX Human thymus BCL-XL.  
XX BCL-XL; apoptosis; cell death; cancer; neurodegenerative disease;  
XX autoimmune disease; Parkinson disease; amyotrophic lateral sclerosis;  
XX multiple sclerosis.  
XX Homo sapiens.  
XX WO9500642-A1.  
XX 05-JAN-1995.  
XX 22-JUN-1994; 94WO-US007089.  
XX 22-JUN-1993; 93US-00081448.  
XX (ARCH-) ARCH DEV CORP.  
XX (UNMI ) UNIV MICHIGAN.  
XX Thompson CB, Boise LH, Nunez G;  
XX WPI; 1995-052079/07.  
XX N-PSDB; AAQ81698.  
XX New poly-nucleotide encoding new poly-peptide(s) that modify apoptosis -  
PT and related vectors, recombinant cells and antibodies, useful in assay  
PT and for control of cell death in e.g. neuronal cells, lymphocytes and  
PT cancers.  
XX Claim 3; Page 94; 127pp; English.

CC This protein may be expressed recombinantly, particularly with pcMV  
CC plasmids as vectors for expression in mammalian cell cultures. The  
CC protein has particular application in cancer cells (failure of programmed  
CC cell death (PCD)) or neurodegenerative and autoimmune diseases (premature  
CC PCD), e.g. Parkinson's disease, amyotrophic lateral sclerosis and  
CC multiple sclerosis. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 233 AA;  
SQ

Query Match 97.7%; Score 1190; DB 2; Length 233;  
Best Local Similarity 97.9%; Pred. No. 5.6e-118;  
Matches 228; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MSQSNRELVDVFLSYKLSQKGYSSQSDVEENRTEAPEETPERETPSAINGNPSWHLA 60  
DB 1 MSQSNRELVDVFLSYKLSQKGYSSQSDVEENRTEAPEETPERETPSAINGNPSWHLA 60

QY 61 DSPAVNGATGHSSSLDAREVIPAQAALREAGDEFEFLRYRRFSDLTSLHITPGTAY 120  
DB 61 DSPAVNGATGHSSSLDAREVIPAQAALREAGDEFEFLRYRRFSDLTSLHITPGTAY 120

QY 121 QSEFQVNNELFRDGVNNGRIVAFPSFGALCVESVDKEMQVLSRIASWMMATYLNHLEP 180  
DB 121 QSEFQVNNELFRDGVNNGRIVAFPSFGALCVESVDKEMQVLSRIASWMMATYLNHLEP 180

QY 181 WIQENGWDTFVDLYGNNAASRKQGERFNRWFLTGMTVAGVVLLGSLFSRK 233  
DB 181 WIQENGWDTFVELYGNNAASRKQGERFNRWFLTGMTVAGVVLLGSLFSRK 233

Db 181 WIQENGWDTFVELYGNNAASRKQGERFNRWFLTGMTVAGVVLGSLFSRK 233

RESULT 9

AAW05821  
ID AAW05821 standard; protein; 233 AA.

AC AAW05821;

DT 30-MAR-1997 (first entry)

DE Bcl-XL protein.

Human; bcl-XL; T-lymphocyte; cell death; BH1 domain; BH2 domain;  
Bcl-2 homology domain; gene therapy; HIV; AIDS; antiense;  
immune disorder; autoimmune disease; graft rejection;  
graft-versus-host disease; apoptosis; adoptive immunotherapy.

OS Homo sapiens.

Key Location/Qualifiers  
Domain 129..148  
/note= "BH1 domain"  
Domain 180..191  
/note= "BH2 domain"

PN W09634956-A1.

XX 07-NOV-1996.

XX 02-MAY-1996; 96WO-US006203.

XX 04-MAY-1995; 95US-00435518.

PR 07-JUN-1995; 95US-00481739.

XX (USNA ) US SEC OF NAVY.

PA (ARCH-) ARCH DEV CORP.

XX June CH, Thompson CB;

XX WPI; 1996-506159/50.

DR N-PSDB; AAT40079.

Inducing or preventing death of T cells by bcl-XL protein regulation -  
used to increase survival of HIV infected cells or to down-regulate  
immune responses in immune diseases.

PS Disclosure; Page 52-53; 76pp; English.

This is the sequence of a human bcl-XL protein, which protects T-  
lymphocytes against cell death. A splice variant form, bcl-XS, lacks a  
stretch of 63 amino acids, and is a dominant negative regulator of bcl-XL  
function. The gene may be modified to facilitate interaction with  
constitulatory Bax protein and inhibit interaction with antagonistic Bad  
protein, by modification of the Bcl-2 homology domains BH1 and/or BH2.  
The bcl-XL gene may be introduced into T-cells in vivo or ex vivo via  
gene transfer using a vector for HIV infection gene therapy, to augment  
intracellular bcl-XL protein levels and protect from cell death. A  
corresponding antisense oligonucleotide or expression vector may be used  
in gene therapy of e.g. autoimmune disease, graft rejection or graft-  
versus-host disease, to induce cell death (e.g. apoptosis) and down-  
regulate the immune response in a T-lymphocyte population

XX Sequence 233 AA;

Query Match 97.7%; Score 1190; DB 2; Length 233;

Best Local Similarity 97.9%; Pred. No. 5.6e-118;

Matches 228; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MSQSNRELVDPLSKLSQKYSQSDVDENRTEAPEETPERTPSAINGNPSWHLA 60

Db 1 MSQSNRELVDPLSKLSQKYSQSDVDENRTEAPEETPERTPSAINGNPSWHLA 60

Qy 61 DSPAVNGATGSHSSSLDAREVI PMAAVKQALREAGDEFELRYRRAFSDLTSLHITPGTAY 120  
Db 61 DSPAVNGATGSHSSSLDAREVI PMAAVKQALREAGDEFELRYRRAFSDLTSLHITPGTAY 120  
Qy 121 QSFQVNVNELFRDGVNNGRIIVAFPSFGALCVESVDKEMQVLVSRIASWMTYNDHLEP 180  
Db 121 QSFQVNVNELFRDGVNNGRIIVAFPSFGALCVESVDKEMQVLVSRIASWMTYNDHLEP 180  
Qy 181 WIQENGWDTFVDLYGNNAASRKQGERFNRWFLTGMTVAGVVLGSLFSRK 233  
Db 181 WIQENGWDTFVELYGNNAASRKQGERFNRWFLTGMTVAGVVLGSLFSRK 233

RESULT 10

AAW31530  
ID AAW31530 standard; protein; 233 AA.

AC AAW31530;

XX 19-FEB-1998 (first entry)

XX Human anti-apoptotic BCL-XL protein.

BCL-XL; anti-apoptotic protein; human; nuclear factor-kappa B;  
NF-kappa B; inhibitor; organ transplant; tissue transplant; inflammation;  
gene therapy; endothelial cell.

OS Homo sapiens.

XX W09730083-A1.

XX 21-AUG-1997.

XX 13-FEB-1997; 97WO-EP000676.

XX 14-FEB-1996; 96US-00601515.

PR 19-APR-1996; 96US-00634995.

XX (NOVS ) NOVARTIS AG.  
PA (NEWE-) NEW ENGLAND DEACONESS HOSPITAL.

XX Bach FH, Ferran C;

XX WPI; 1997-424975/39.

Recombinant endothelial cell containing DNA encoding anti-apoptotic  
protein - is less susceptible to inflammatory response and is useful for  
generating tissues or organs for transplantation.

PS Claim 6; Page 46; 75pp; English.

This protein sequence comprises human BCL-XL, a protein capable of  
blocking or suppressing NF-kappa B (NF-kB) activation. A claimed method  
of genetically modifying a mammalian endothelial cell to render it less  
susceptible to an inflammatory or other immunological stimulus comprises  
inserting into the cell, DNA encoding an anti-apoptotic protein able to  
inhibit NF-kB, and expressing the cell such that NF-kB activation of the  
cell is inhibited in the presence of the cellular activating  
stimulus. Suitable anti-apoptotic proteins include A20 (see AAW31528),  
BCL-2 (see AAW31529), BCL-XL and A1 (see AAW31531) and their deletion  
mutants capable of inhibiting NF-kB, such as polypeptides comprising  
amino acid residues 5-24, 86-100, 129-148 and 180-195 of BCL-XL. Also  
claimed are: (1) a mammalian endothelial cell modified by the above  
method; and (2) a non-human transgenic or somatic recombinant mammal  
comprising DNA encoding an anti-apoptotic protein of a different species.  
The method can be used to generate donor endothelial cells or graftable  
tissues or organs for transplantation into recipient species

XX Sequence 233 AA;

Query Match 97.7%; Score 1190; DB 2; Length 233;

Best Local Similarity 97.9%; Pred. No. 5.6e-118;

Matches 228; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MSQSNRELVDVFLSYKLSQKGYWSQSDVEENRTEAPEETEPEPESAINGNPSWHLA 60  
 Dd 1 MSQSNRELVDVFLSYKLSQKGYWSQSDVEENRTEAPEETEPEPESAINGNPSWHLA 60  
 Qy 61 DSPAVNGATGHSSSLDAREVPMMAVKQALREAGDEFELRYRRAPSDLTSQLHITPGTAY 120  
 Dd 61 DSPAVNGATGHSSSLDAREVPMMAVKQALREAGDEFELRYRRAPSDLTSQLHITPGTAY 120  
 Qy 121 QSFQVNVNELFRDGVNMGRIVAFPSFGALCVESVDKEMQVLVSRIASWMAATYLNHLEP 180  
 Dd 121 QSFQVNVNELFRDGVNMGRIVAFPSFGALCVESVDKEMQVLVSRIASWMAATYLNHLEP 180  
 Qy 181 WIQENGGWDTFVLYGNNAASRKQGERFNRWFLTGMTVAGVVLGSLFSRK 233  
 Dd 181 WIQENGGWDTFVLYGNNAASRKQGERFNRWFLTGMTVAGVVLGSLFSRK 233

RESULT 11  
 ADE62493  
 ID ADE62493 standard; protein; 233 AA.  
 XX AC ADE62493;  
 XX DT 29-JAN-2004 (first entry)  
 XX Human Protein Q07817, SEQ ID NO 8422.  
 DE Human; pain; neuronal tissue; gene therapy;  
 KW spinal segmental nerve injury; chronic constriction injury; CCI;  
 KW spared nerve injury; SNI; Chung.  
 XX OS Homo sapiens.  
 XX WO2003016475-A2.  
 XX 27-FEB-2003.  
 XX 14-AUG-2002; 2002WO-US025765.  
 XX 14-AUG-2001; 2001US-0312147P.  
 PR 01-NOV-2001; 2001US-0346382P.  
 PR 26-NOV-2001; 2001US-0333347P.  
 XX (GEO) GEN HOSPITAL CORP.  
 PA (FARB) BAYER AG.  
 XX Woolf C, D'urso D, Befort K, Costigan M;  
 PI WPI; 2003-268312/26.  
 DR GENBANK; Q07817.  
 XX New composition comprising two or more isolated polypeptides, useful for  
 PT preparing a medicament for treating pain in an animal.  
 XX Claim 1; Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat  
 CC or human polynucleotides or a polynucleotide which represents a fragment,  
 CC derivative or allelic variation of the nucleic acid sequence. Also  
 CC claimed are a vector comprising the novel polynucleotide, a host cell  
 CC comprising the vector, a method for identifying a nucleotide sequence  
 CC which is differentially regulated in an animal subjected to pain and a  
 CC kit to perform the method, an array, a method for identifying an agent  
 CC that increases or decreases the expression of the polynucleotide sequence  
 CC that is differentially expressed in neuronal tissue of a first animal  
 CC subjected to pain, a method for identifying a compound which regulates  
 CC the expression of a polynucleotide sequence which is differentially  
 CC expressed in an animal subjected to pain, a method for identifying a  
 CC compound that regulates the activity of one or more of the  
 CC polynucleotides, a method for producing a pharmaceutical composition, a  
 CC method for identifying a compound or small molecule that regulates the  
 CC activity in an animal of one or more of the polypeptides given in the

CC specification, a method for identifying a compound useful in treating  
 CC pain and a pharmaceutical composition comprising the one or more  
 CC polypeptides or their antibodies. The polynucleotide or the compound that  
 CC modulates its activity is useful for preparing a medicament for treating  
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
 CC therapy). The sequence presented is a human protein (shown in Table 2 of  
 CC the specification) which is differentially expressed during pain. Note:  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic form directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.  
 XX Sequence 233 AA;

Query Match 97.7%; Score 1190; DB 7; Length 233;  
 Best Local Similarity 97.9%; Pred. No. 5.6e-118;  
 Matches 228; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
 Qy 1 MSQSNRELVDVFLSYKLSQKGYWSQSDVEENRTEAPEETEPEPESAINGNPSWHLA 60  
 Dd 1 MSQSNRELVDVFLSYKLSQKGYWSQSDVEENRTEAPEETEPEPESAINGNPSWHLA 60  
 Qy 61 DSPAVNGATGHSSSLDAREVPMMAVKQALREAGDEFELRYRRAPSDLTSQLHITPGTAY 120  
 Dd 61 DSPAVNGATGHSSSLDAREVPMMAVKQALREAGDEFELRYRRAPSDLTSQLHITPGTAY 120  
 Qy 121 QSFQVNVNELFRDGVNMGRIVAFPSFGALCVESVDKEMQVLVSRIASWMAATYLNHLEP 180  
 Dd 121 QSFQVNVNELFRDGVNMGRIVAFPSFGALCVESVDKEMQVLVSRIASWMAATYLNHLEP 180  
 Qy 181 WIQENGGWDTFVLYGNNAASRKQGERFNRWFLTGMTVAGVVLGSLFSRK 233  
 Dd 181 WIQENGGWDTFVLYGNNAASRKQGERFNRWFLTGMTVAGVVLGSLFSRK 233

RESULT 12  
 ADM45995  
 ID ADM45995 standard; protein; 233 AA.  
 XX AC ADM45995;  
 XX DT 03-JUN-2004 (first entry)  
 XX Human apoptosis inhibitory factor Bcl-xL protein.  
 DE random oligonucleotide library; protein interaction; ligand;  
 KW receptor binding site; human; apoptosis inhibitory factor; Bcl-xL.  
 XX OS Homo sapiens.  
 XX JP2004024078-A.  
 XX 29-JAN-2004.  
 XX 24-JUN-2002; 2002JP-00183456.  
 XX 24-JUN-2002; 2002JP-00183456.  
 XX (SERE-) SERESUTA REKISHIKO SCI KK.  
 XX WPI; 2004-161478/16.  
 XX N-PSDB; ADM45994.  
 XX Random oligonucleotide useful for detecting protein interaction, having  
 PT base sequence, where each base of 1st and 2nd of the codon is the any of  
 PT G, C, T (U), or A and the base of 3rd of codon is G or C, or G or T (U).  
 XX Example 2; SEQ ID NO 4; 43pp; Japanese.  
 XX The invention relates to a novel random oligonucleotide having a base  
 CC sequence where each base of the 1st and 2nd codon is any of G, C, T (U)  
 CC or A and each base of the 3rd codon is G or C, or G or T (U). The methods  
 CC of the invention may be useful for preparing a random oligonucleotide

CC preparation to be used for detecting protein interactions or for  
 CC screening ligand or receptor protein binding sites. The current sequence  
 CC is that of the human apoptosis inhibitory factor Bcl-xL protein of the  
 CC invention.

XX SQ Sequence 233 AA;  
 Query Match 97.7%; Score 1190; DB 8; Length 233;  
 Best Local Similarity 97.9%; Pred. No. 5,6e-118;  
 Matches 228; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
 Qy 1 MSQSNRELVDVFLSYKLSQKGYNSQFSDVEENRTEAPEETEPEPTPSAINGNPSWHLA 60  
 Db 1 MSQSNRELVDVFLSYKLSQKGYNSQFSDVEENRTEAPEETEPEPTPSAINGNPSWHLA 60  
 Qy 61 DSPAVNGATGHSSSLDAREVTPMAAVKQALREAGDEPELRYRRAPFSDLTSLQHTTPGTAY 120  
 Db 61 DSPAVNGATGHSSSLDAREVTPMAAVKQALREAGDEPELRYRRAPFSDLTSLQHTTPGTAY 120  
 Qy 121 QSFQVNVNELFRDGVNMGRIVAFPSFGALCVESVDKEMQVLVSRIASWMTYLNHLEP 180  
 Db 121 QSFQVNVNELFRDGVNMGRIVAFPSFGALCVESVDKEMQVLVSRIASWMTYLNHLEP 180  
 Qy 181 WIQENGWDTFVDLYGNNAAESRKQGERFNRWFLTGMTVAGVVLGSLFSRK 233  
 Db 181 WIQENGWDTFVELYGNNAAESRKQGERFNRWFLTGMTVAGVVLGSLFSRK 233

RESULT 13  
 ADN04261  
 ID ADN04261 standard; protein; 233 AA.  
 XX  
 AC ADN04261;  
 DT 01-JUL-2004 (first entry)  
 XX  
 DE Antipsoriatic protein sequence #325.  
 XX  
 KW antipsoriatic; gene therapy; psoriasis; diagnosis.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2004028479-A2.  
 XX  
 PD 08-APR-2004.  
 XX  
 XX 25-SEP-2003; 2003WO-US030907.  
 XX  
 XX 25-SEP-2002; 2002US-0414006P.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 XX Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WI;  
 PI Wu TD;  
 XX  
 XX WPI; 2004-305105/28.  
 DR N-PSDB; ADN04260.  
 XX  
 XX New PRO nucleic acid or polypeptide, useful for preparing a  
 PT pharmaceutical composition for diagnosing or treating psoriasis in a  
 PT mammal.  
 XX  
 XX Claim 9; SEQ ID NO 655; 3069pp; English.  
 FS  
 XX The invention relates to novel polynucleotide and polypeptides for  
 CC treating psoriasis or a sequence having at least 80% identity to the  
 CC above sequences. The nucleic acid is useful for preparing a composition  
 CC for diagnosing or treating psoriasis in a mammal. This sequence  
 CC corresponds to one of the polypeptides of the invention.  
 XX  
 SQ Sequence 233 AA;  
 Query Match 97.7%; Score 1190; DB 8; Length 233;

Best Local Similarity 97.9%; Pred. No. 5,6e-118;  
 Matches 228; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
 Qy 1 MSQSNRELVDVFLSYKLSQKGYNSQFSDVEENRTEAPEETEPEPTPSAINGNPSWHLA 60  
 Db 1 MSQSNRELVDVFLSYKLSQKGYNSQFSDVEENRTEAPEETEPEPTPSAINGNPSWHLA 60  
 Qy 61 DSPAVNGATGHSSSLDAREVTPMAAVKQALREAGDEPELRYRRAPFSDLTSLQHTTPGTAY 120  
 Db 61 DSPAVNGATGHSSSLDAREVTPMAAVKQALREAGDEPELRYRRAPFSDLTSLQHTTPGTAY 120  
 Qy 121 QSFQVNVNELFRDGVNMGRIVAFPSFGALCVESVDKEMQVLVSRIASWMTYLNHLEP 180  
 Db 121 QSFQVNVNELFRDGVNMGRIVAFPSFGALCVESVDKEMQVLVSRIASWMTYLNHLEP 180  
 Qy 181 WIQENGWDTFVDLYGNNAAESRKQGERFNRWFLTGMTVAGVVLGSLFSRK 233  
 Db 181 WIQENGWDTFVELYGNNAAESRKQGERFNRWFLTGMTVAGVVLGSLFSRK 233

RESULT 14  
 ADO19867  
 ID ADO19867 standard; protein; 233 AA.  
 XX  
 AC ADO19867;  
 DT 12-AUG-2004 (first entry)  
 XX  
 DE Human PRO polypeptide #394.  
 XX  
 KW Human; PRO; immune related disorder; systemic lupus erythematosus;  
 KW rheumatoid arthritis; osteoarthritis; juvenile chronic arthritis;  
 KW systemic sclerosis; Sjogren's syndrome; vasculitis; sarcoidosis;  
 KW autoimmune haemolytic anaemia; autoimmune thrombocytopenia; thyroiditis;  
 KW diabetes mellitus; renal disease; demyelinating disease;  
 KW central nervous system; peripheral nervous system;  
 KW demyelinating polyneuropathy; Guillain-Barre syndrome;  
 KW chronic inflammatory demyelinating polyneuropathy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2004043361-A2.  
 XX  
 PD 27-MAY-2004.  
 XX  
 XX 06-NOV-2003; 2003WO-US035268.  
 PF  
 XX 08-NOV-2002; 2002US-0425235P.  
 PR  
 XX (GETH ) GENENTECH INC.  
 PA  
 XX Fong S, Dennis K, Clark H, Chiu H, Schoenfeld J, Williams PM;  
 PI Wood WI, Wu TD;  
 XX  
 XX WPI; 2004-420067/39.  
 DR N-PSDB; ADO19866.  
 XX  
 XX Novel PRO polypeptide e.g., PRO69614, PRO71106, or PRO86388 useful for  
 PT treating an immune related disorder such as systemic lupus erythematosus,  
 PT rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or  
 PT spondyloarthropathy.  
 XX  
 XX Claim 7; SEQ ID NO 788; 1731pp; English.  
 FS  
 XX The invention relates to human PRO polypeptides and the polynucleotides  
 CC encoding them. The polypeptides and polynucleotides are useful for  
 CC treating and diagnosing immune related disorders in mammals. The immune  
 CC related disorders include systemic lupus erythematosus, rheumatoid  
 CC arthritis, osteoarthritis, juvenile chronic arthritis, systemic  
 CC sclerosis, Sjogren's syndrome, vasculitis, sarcoidosis, autoimmune  
 CC haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes  
 CC mellitus, immune-mediated renal disease, demyelinating diseases of the  
 CC central or peripheral nervous system, demyelinating polyneuropathy.

CC Guillain-Barre syndrome and chronic inflammatory demyelinating  
CC polyneuropathy. This sequence represents a human PRO polypeptide of the  
CC invention.  
XX  
SQ Sequence 233 AA;

Query Match 97.7%; Score 1190; DB 8; Length 233;  
Best Local Similarity 97.9%; Pred. No. 5.6e-118;  
Matches 228; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MSQSNRELVDVFLSYKLSQKGYSSQFSDVEENRTEAPEETEPETPSAINGNPSWHLA 60  
Db 1 MSQSNRELVDVFLSYKLSQKGYSSQFSDVEENRTEAPEETEPETPSAINGNPSWHLA 60

Qy 61 DSPAVNGATGHSSSLDAREVPMVAVKQALREAGDEFEELRYRRAFSDLTSLHITPGTAY 120  
Db 61 DSPAVNGATGHSSSLDAREVPMVAVKQALREAGDEFEELRYRRAFSDLTSLHITPGTAY 120

Qy 121 QSPQVNVNELFRDGVNNGRIVAFPSFGALCVESVDKEMQVLVSRIASWMTYLNHLEP 180  
Db 121 QSPQVNVNELFRDGVNNGRIVAFPSFGALCVESVDKEMQVLVSRIASWMTYLNHLEP 180

Qy 181 WIQENGWDTFVDLYGNNAAESRKQGERFNRWFLTGMTVAGVVLGSLFSRK 233  
Db 181 WIQENGWDTFVELYGNNAAESRKQGERFNRWFLTGMTVAGVVLGSLFSRK 233

RESULT 15  
ABM82217  
ID ABM82217 standard; protein; 233 AA.  
AC  
XX  
XX  
DT 18-NOV-2004 (first entry)  
XX  
XX  
DE Tumour-associated antigenic target (TAT) polypeptide PRO33141, SEQ:5714.  
XX  
KW Tumour-associated antigenic target; TAT; human; overexpression; cancer;  
KW tumour; diagnosis; cell proliferative disorder; breast cancer;  
KW colorectal cancer; lung cancer; ovarian cancer; liver cancer;  
KW central nervous system cancer; bladder cancer; pancreatic cancer;  
KW cervical cancer; melanoma; leukaemia; hybridisation probe;  
KW chromosome identification; chromosome mapping; gene mapping;  
KW gene therapy; cytostatic.  
XX  
XX Homo sapiens.  
XX  
XX WO2004030615-A2.  
XX  
XX 15-APR-2004.  
XX  
XX 29-SEP-2003; 2003WO-US028547.  
XX  
XX 02-OCT-2002; 2002US-0414971P.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
XX Wu TD, Zhang Z, Zhou Y;  
XX  
XX WPI; 2004-347921/32.  
XX  
XX N-ESDB; ACN40740.  
XX  
XX New tumor-associated antigenic target polypeptides and nucleic acids,  
XX useful in preparing a medicament for treating or detecting a  
XX proliferative disorder, e.g. breast, lung, colorectal, ovarian or  
XX prostate cancer or tumor.  
XX  
XX Claim 12; SEQ ID NO 5714; 7273pp; English.  
XX  
XX The invention relates to human tumour-associated antigenic target (TAT)  
XX polypeptides, and their related nucleic acids. The TAT polypeptides are  
XX overexpressed in cancer tissues compared to normal tissues, and may thus  
XX serve as effective targets for the diagnosis and treatment of cancer in

CC mammals. The invention also relates to nucleic acid and polypeptide  
CC sequences at least 80% identical to the TAT nucleic acids and  
CC polypeptides; expression vectors and host cells comprising a TAT nucleic  
CC acid; an antibody specific for a TAT polypeptide; a peptide or organic  
CC molecule which binds to a TAT polypeptide; fusion proteins comprising a  
CC TAT polypeptide, and methods and compositions for the treatment or  
CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,  
CC antibodies, antagonists, binding molecules and compositions are useful  
CC for diagnosing or treating a cell proliferative disorder associated with  
CC increased TAT expression, particularly cancers such as breast cancer,  
CC colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder  
CC cancer, pancreatic cancer, cervical cancer, cancers of the central  
CC nervous system, melanoma and leukaemia. TAT nucleic acids may further be  
CC used as hybridisation probes, in chromosome and gene mapping, in  
CC chromosome identification and in gene therapy. The present sequence  
CC represents a TAT polypeptide of the invention  
XX  
SQ Sequence 233 AA;

Query Match 97.7%; Score 1190; DB 8; Length 233;  
Best Local Similarity 97.9%; Pred. No. 5.6e-118;  
Matches 228; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MSQSNRELVDVFLSYKLSQKGYSSQFSDVEENRTEAPEETEPETPSAINGNPSWHLA 60  
Db 1 MSQSNRELVDVFLSYKLSQKGYSSQFSDVEENRTEAPEETEPETPSAINGNPSWHLA 60

Qy 61 DSPAVNGATGHSSSLDAREVPMVAVKQALREAGDEFEELRYRRAFSDLTSLHITPGTAY 120  
Db 61 DSPAVNGATGHSSSLDAREVPMVAVKQALREAGDEFEELRYRRAFSDLTSLHITPGTAY 120

Qy 121 QSPQVNVNELFRDGVNNGRIVAFPSFGALCVESVDKEMQVLVSRIASWMTYLNHLEP 180  
Db 121 QSPQVNVNELFRDGVNNGRIVAFPSFGALCVESVDKEMQVLVSRIASWMTYLNHLEP 180

Qy 181 WIQENGWDTFVDLYGNNAAESRKQGERFNRWFLTGMTVAGVVLGSLFSRK 233  
Db 181 WIQENGWDTFVELYGNNAAESRKQGERFNRWFLTGMTVAGVVLGSLFSRK 233

Search completed: March 31, 2005, 00:28:16  
Job time : 169.1 secs

100



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OM nucleic - nucleic search, using sw model

Run on: March 31, 2005, 00:31:02 ; Search time 7391 Seconds  
(without alignments)  
11420.510 Million cell updates/sec

Title: US-10-049-822A-1  
Perfect score: 1742  
Sequence: 1 cacagacagaccagctgag.....ggagccctggggcttcct 1742

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- GenEmbl.\*  
1: gb\_ba.\*  
2: gb\_hcg.\*  
3: gb\_in.\*  
4: gb\_on.\*  
5: gb\_ov.\*  
6: gb\_pat.\*  
7: gb\_ph.\*  
8: gb\_pl.\*  
9: gb\_pr.\*  
10: gb\_ro.\*  
11: gb\_sts.\*  
12: gb\_sy.\*  
13: gb\_un.\*  
14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1742	100.0	1742	6	BD012974 A mutagen
2	1742	100.0	1742	6	BD013799 Modified
3	1742	100.0	1742	10	U72350 Rattus norv
4	1662.2	95.4	2232	10	X82537 R.norvegicu
5	1240.6	71.2	172803	2	AC147787 Rattus no
6	1240.6	71.2	227938	2	AC098008 Rattus no
7	1168	67.0	1466	6	AX775078 Sequence
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ALIGNMENTS

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DEFINITION A mutagenized rat bcl-x cDNA and a modified protein therefrom.  
ACCESSION BD012974  
VERSION BD012974.1 GI:22093163  
KEYWORDS WO 0112807-A/1.  
SOURCE Rattus norvegicus (Norway rat)  
ORGANISM Rattus norvegicus  
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.  
REFERENCE 1 (bases 1 to 1742)  
AUTHORS Ota,S. and Aso,S.  
TITLE A mutagenized rat bcl-x cDNA and a modified protein therefrom  
JOURNAL Patent: WO 0112807-A 1 22-FEB-2001;  
JAPAN SCIENCE AND TECHNOLOGY CORP, SHIGEO OTA, SADAMITSU ASO  
COMMENT OS Rattus norvegicus (rat)  
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PD 22-FEB-2001  
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DEFINITION 1742 bp DNA linear PAT 27-AUG-2002  
ACCESSION BD013799  
VERSION BD013799 1 GI:22554128  
KEYWORDS JP 2001120281-A/1.  
SOURCE Rattus norvegicus (Norway rat)  
ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.  
REFERENCE 1 (bases 1 to 1742)  
Ota, S. and Abo, S.  
Modified cDNA of rat bcl-x gene and modified protein  
TITLE Patent: JP 2001120281-A 1 08-MAY-2001;  
JOURNAL JAPAN SCIENCE AND TECHNOLOGY CORP  
COMMENT OS Rattus norvegicus (rat)  
PN JP 2001120281-A/1  
PD 08-MAY-2001  
PF 16-AUG-2000 JP 2000246999  
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PC (C12P21/02, C12R1:19), (C12P21/02, C12R1:91), C12N15/00, C12N5/00  
CC Modified cDNA of rat bcl-x gene and modified protein FH Key  
Location/Qualifiers (72). (773).  
FT CDS  
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 MEDLINE  
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 PUBLISHED  
 2 (bases 1 to 1742)  
 REFERENCES  
 Shiraiwa,N., Inohara,N., Okada,S., Yuzaki,M., Shoji,S. and Ohta,S.  
 Direct Submission  
 Submitted (24-SEP-1996) Division of Biochemistry, Institute of  
 Gerontology, 1-396 Kosugi-cho, Nakahara-ku, Kawasaki City 211,  
 Japan

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VERSION X82537.1 GI:607176
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 2232)
AUTHORS Michaelidis, T.M.
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2232)
AUTHORS Michaelidis, T.M.
TITLE Direct Submission
JOURNAL Submitted (04-NOV-1994) T.M. Michaelidis, Max-Planck-Inst. for
Psychiatry, Dept of Neurochemistry, 82152 Martinsried, FRG
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Matches 1516; Conservative 0; Mismatches 29; Indels 208; Gaps 5;									
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Qy	361	TTGAACTGCGGTACCGGAGAGCATTCAGTGATCTTAACATCCAGCTTCATATAACCCAG	420						
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Qy	1141	GAGAGCTCTCTAAACCTCTTCCCCCAGAGACTAGATTGCCCTTGGTTTGTGTGTGC	1200
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Qy	1610	GCCTCATCTTCTCAAGATCAGCTGTGGGCAATCTTTGCTTTGGGTGTGGGCCACAGGGTTC	1669
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PF01111717

RESULT	AC098008	227938 bp	DNA	linear	HTG 10-MAY-2003
LOCUS	Rattus norvegicus clone CH230-106A2,				
DEFINITION					WORKING DRAFT SEQUENCE.
ACCESSION	AC098008				
VERSION	AC098008.6	GI:30521376			
KEYWORDS	HTG; HTGS PHASE2; HTGS DRAFT; HTGS_FULLTOP.				
SOURCE	Rattus norvegicus	(Norway rat)			
ORGANISM	Rattus norvegicus				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;				
	Rattus.				





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[illegible]

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Qy	301	CGCGGAGGTAATCCCATCGCAGCAGTGAAGCAAGCGCTGAGAGAGGCTGGCGATGAGT	360
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Qy	961	CACCTTCCCCCACAATCTCAGTTCCCTTGGCTCAAAACTCACAGGTTTTCCTCAGAT	1020
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Qy	1320	AAATGCAGGCTGTCTGGGATAACAGGCAAG-----ACCTCCTCCCCACCTGTGGCCT	1373
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MMU51278			
LOCUS	MMU51278	1466 bp	mRNA linear ROD 21-NOV-1997
DEFINITION	Mus musculus thymus Bcl-XL mRNA, complete cds.		
ACCESSION	U51278		
VERSION	U51278.1	GI:2636673	
KEYWORDS			
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.		
AUTHORS	Yang,X.F., Weber,G.F. and Cantor,H.		
TITLE	A novel Bcl-x isoform connected to the T cell receptor regulates apoptosis in T cells		
JOURNAL	Immunity 7 (5), 629-639 (1997)		
MEDLINE	98051053		
PUBMED	9390687		
REFERENCE	2 (bases 1 to 1466)		
AUTHORS	Yang,X.-P. and Cantor,H.		
TITLE	Direct Submission		
JOURNAL	Submitted (13-MAR-1996) Xiao-Fang Yang, Immunopathology, Dana-Farber Cancer Institute, 44 Binney Street, Boston, MA 02115.		
FEATURES	source		
CDS	Location/Qualifiers 1..1466 /organism="Mus musculus" /mol_type="mRNA" /strain="B6/CBA" /db_xref="taxon:10090" /tissue_type="thymus" 103..804 /note="Bcl-x long form" /codon_start=1 /product="Bcl-XL" /protein_id="AAC53459.1" /db_xref="GI:2636674" /translation="MSQSRELVDPLSYKLSOKYSWSQFSVEENRTEAPEETEAERFPTSANGNPSWHLADSPAVNGATGHSSLDAREVIPIAAVKQAUREAGDEFLRYRRAFDSDITSLQHITPTGYOSFEQVNNELFRDGWNVGRIVAFFSGALICVESYDKEMQVLVSRTASWMATYLNDHLESPWIQENGWDFTVDLYGNNAAEESRKKGEGFNRFLLTGM TVAGVVILGLSLFRSK"		
ORIGIN			
Query Match	67.0%; Score 1168;	DB 10;	Length 1466;
Best Local Similarity	91.0%;	Pred. No. 0;	
Matches 1331;	Conservative 0;	Mismatches 95;	Indels 36; Gaps 7;
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Qy	61	CTATTATATAAAATGCTCTCAGACGAACCGGAGCTGGTGGTTCCTCTCTCAAGAAGC	120
Db	92	CTATTATATAAAATGCTCTCAGACGAACCGGAGCTGGTGGTTCCTCTCTCAAGAAGC	151
Qy	121	TCTCCCAAGAAGGATACAGCTGGAGTCAGTTTACGAGATGCGAAGAAACAGACTGAAG	180
Db	152	TTTCCCAAGAAGGATACAGCTGGAGTCAGTTTACGAGATGCGAAGAAATGAGCTGAGG	211



Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wlezyk, R., Wood, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhauser, A., Weiss, R., Smith, D. R., Holt, R. A., Smith, H. O., Weinstock, G. and Gibbs, R. A.

Direct Submission  
Unpublished  
2 (bases 1 to 224136)  
Rat Genome Sequencing Consortium.  
Submitted (09-SEP-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
3 (bases 1 to 224136)  
Rat Genome Sequencing Consortium.  
Direct Submission  
Submitted (20-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
On Nov 20, 2002 this sequence version replaced gi:22759158.  
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center  
Center: Baylor College of Medicine  
Center code: BCM  
Web site: <http://www.hgsc.bcm.tmc.edu/>  
Contact: hgsc-help@bcm.tmc.edu  
----- Project Information  
Center project name: KBNV  
Center clone name: CH230-319B8  
----- Summary Statistics  
Assembly program: Phrap; version 0.990329  
Consensus quality: 215274 bases at least Q40  
Consensus quality: 217755 bases at least Q30  
Consensus quality: 218840 bases at least Q20  
Estimated insert size: 224934; sum-of-contigs estimation  
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation

\* NOTE: Estimated insert size may differ from sequence length  
(see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)).  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 1 contigs. Gaps between the contigs  
\* are represented as runs of N. The order of the pieces  
\* is believed to be correct as given, however the sizes  
\* of the gaps between them are based on estimates that have  
\* provided by the submitter.  
\* This sequence will be replaced  
\* by the finished sequence as soon as it is available and  
\* the accession number will be preserved.

\* 1 224136: contig of 224136 bp in length.  
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misc\_feature

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Best Local Similarity	99.8%; Pred. No. 1e-303;	Best Local Similarity	99.8%; Pred. No. 1e-303;
Matches 1107; Conservative	0; Mismatches	Matches 1107; Conservative	0; Mismatches
2;	Indels	2;	Indels
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Qy	695 GCGTTTCAACCGCTGGTTCTCTGACGGGCATGACTGTGGCTGGTGTAGTTCTGCTGGGCTC	Qy	695 GCGTTTCAACCGCTGGTTCTCTGACGGGCATGACTGTGGCTGGTGTAGTTCTGCTGGGCTC
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DEFINITION
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VERSION 1.0
KEYWORDS HTG; HTGS PHASE1; HTGS DRAFT; HTGS_ENRICHED.
SOURCE Rattus norvegicus (Norway rat)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
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Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O.,
Weinstock, G. and Gibbs, R.A.
Direct Submission
Unpublished
2 (bases 1 to 249872)
Worley, K.C.
Direct Submission
Submitted (12-JAN-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 249872)
Rat Genome Sequencing Consortium.
Direct Submission
Submitted (10-MAY-2003) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On May 10, 2003 this sequence version replaced gi:24954343.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
table.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GHKL
Center clone name: CH230-137H11
----- Summary Statistics
Assembly program: Atlas 3.0
Consensus quality: 232472 bases at least Q40
Consensus quality: 235092 bases at least Q30
Consensus quality: 236668 bases at least Q20
Estimated insert size: 242767; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
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* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 8 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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* 244647 244746: gap of unknown length

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## TITLE

JOURNAL

## REFERENCE

AUTHORS

## TITLE

JOURNAL

## REFERENCE

AUTHORS

## TITLE

JOURNAL

## COMMENT

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REFERENCE 1			
AUTHORS			
TITLE			
JOURNAL			
IMPERIAL COLLEGE OF SCIENCE, TECHNOLOGY & MEDICINE (GB)			
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LOCUS BC019307 2575 bp mRNA linear PRI 29-JUN-2004  
DEFINITION Homo sapiens BC12-like 1, transcript variant 1, mRNA (cdna clone  
MGC:4204 IMAGE:2823498), complete cds.

## ACCESSION

BC019307

## VERSION

BC019307.1 GI:17939633

## KEYWORDS

MGC.

## SOURCE

Homo sapiens (human)

## ORGANISM

Homo sapiens

## REFERENCE

1 (bases 1 to 2575)

## AUTHORS

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,  
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,  
Altschul, S.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Bhat, N.K.,  
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Bhat, N.K.,  
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,  
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,  
Scheetz, T.E., Brownstein, M.J., Ustin, T.B., Toshiyuki, S.,  
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,  
Abramson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J.,  
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,  
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,  
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,  
Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S.,  
Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y.,  
Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D.,  
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,  
Butterfield, Y.S., Krzywicki, M.I., Skalska, U., Smaluk, D.E.,  
Schnurch, A., Schein, J.B., Jones, S.J. and Marra, M.A.

## TITLE

Generation and initial analysis of more than 15,000 full-length  
human and mouse cDNA sequences

## JOURNAL

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

## PUBMED

12477932

## REFERENCE

2 (bases 1 to 2575)

## AUTHORS

Strausberg, R.

## TITLE

Direct Submission

## JOURNAL

Submitted (13-DEC-2001) National Institutes of Health, Mammalian  
Gene Collection (MGC), Cancer Genomics Office, National Cancer  
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
USA





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KEYWORDS
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ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE 1 (bases 1 to 1235)
AUTHORS Fang, W., Rivard, J.J., Mueller, D.L. and Behrens, T.W.
TITLE Cloning and molecular characterization of mouse bcl-x in B and T
lymphocytes
JOURNAL J. Immunol. 153 (10), 4388-4398 (1994)
MEDLINE 95052604
PUBMED 7963517
REFERENCE 2 (bases 1 to 1235)
AUTHORS Behrens, T.W.
TITLE Direct Submission
JOURNAL Submitted (26-MAY-1994) Timothy W. Behrens, Medicine, University of
Minnesota, 515 Delaware St. S.E., Minneapolis, MN 55455, USA
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 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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 1 (bases 1 to 157220)  
 Almeida, J.

Direct Submission  
 Submitted (31-MAY-2002) Wellcome Trust Sanger Institute, Hinxton,  
 Cambridgeshire, CB10 1SA, UK. E-mail enquiries:  
 humquere@sanger.ac.uk  
 On Jun 21, 2002 this sequence version replaced gi:21104246.  
 During sequence assembly data is compared from overlapping clones.  
 Where differences are found these are annotated as variations  
 together with a note of the overlapping clone name. Note that the  
 variation annotation may not be found in the sequence submission  
 corresponding to the overlapping clone, as we submit sequences with  
 only a small overlap as described above.  
 This sequence was finished as follows unless otherwise noted: all  
 regions were either double-stranded or sequenced with an alternate  
 chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such  
 as compressions and repeats; all regions were covered by at least  
 one plasmid subclone or more than one M13 subclone; and the  
 assembly was confirmed by restriction digest. The following  
 abbreviations are used to associate primary accession numbers given  
 in the feature table with their source databases: Em, EMBL; Sw,  
 SWISSPROT; Tr, TrEMBL; Wp, WORMPEP; Information on the WORMPEP  
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 from the RPCI-23 Mouse PAC Library  
 constructed by the group of Pieter de Jong.  
 For further details see http://www.chori.org/bacpac/home.htm  
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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11294.841 Million cell updates/sec

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 3: Geneseqn2000s:\*
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- 12: Geneseqn2004as:\*
- 13: Geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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2	1168	67.0	1466	10	Ade85177 Farnesyl
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5	1038.2	59.6	2575	13	Adp54991 Human PRO
6	1038.2	59.6	2575	13	Adp24509 PRO polyp
7	1038.2	59.6	2598	12	Adq97765 Human can
8	811.6	46.6	71594	12	Adq97761 Mouse can
9	787.8	45.2	863	12	Adh52632 Chinese h
10	741	42.5	926	2	Aag81698 Human thy
11	741	42.5	926	2	Aat40079 Bcl-XL ge
12	737.8	42.4	926	3	Aaz93614 Bcl-x-gen
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20	737.8	42.4	926	12	Adh52630 Human ant

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26	703.6	40.4	7436	13	Ado80675	Ado80675 Bcl-XL ex
27	690.8	39.7	702	13	Ado80676	Ado80676 Rat anti-
28	661.4	38.0	2386	10	Adg89403	Adg89403 Cancer de
29	661.4	38.0	2386	12	Adn04260	Adn04260 Antipsori
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## ALIGNMENTS

## RESULT 1

AAF75960  
ID AAF75960 standard; cDNA; 1742 BP.

XX AAF75960;

DT 22-MAY-2001 (first entry)

XX Rat wild-type Bcl-xL cDNA.

Rat Bcl-xL; apoptosis inhibitor; programmed cell death inhibitor;  
wild-type; antiapoptotic; cell death-associated disease;  
tissue transplant preservative; ss.

OS Rattus norvegicus.

XX WO200112807-A1.

PD 22-FEB-2001.

XX 17-AUG-2000; 2000WO-JP005502.

XX 17-AUG-1999; 99JP-00230642.

XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.

PI Ohta S; Asoh S;

XX WPI; 2001-211219/21.

DR P-FSDB; AAB73303.

XX Modified cDNA of rat bcl-x gene and encoded protein with membrane permeability to enhance uptake for effective inhibition of cell death e.g. apoptosis, useful in remedies for diseases associated with cell death.

XX Claim 1; Page 43-45; 56pp; Japanese.

XX The invention relates to a mutant rat Bcl-x protein and the cDNA encoding it. The mutant rat Bcl-x protein (Bcl-xFNK) has the substitutions Y22F, Q26N, and R155K relative to the wild-type Bcl-xL protein. The invention also encompasses recombinant vectors and host cells comprising the modified nucleic acid sequence. The mutant Bcl-x protein is able to

permeate the cell membrane, thus enhancing its ability to be taken up into a cell and to act as an inhibitor of apoptosis (programmed cell death). Bcl-2, Bcl-XL and nucleic acids encoding it are useful in remedies for diseases associated with cell death and in additives for maintaining the stability of transplanted cells and organs. The present sequence represents cDNA encoding wild-type rat Bcl-XL.

SQ Sequence 1742 BP; 377 A; 507 C; 477 G; 381 T; 0 U; 0 Other;

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Best Local Similarity 100.0%; Pred. No. 0;

Matches 1742; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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7

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QY 181 CCCAGAAGAACTGAACCAAGGAGACCCCAGTGCCATCAATGGCAACCATCCT 240

Year	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100
1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	

Qy 241 GGCACTGGCGGATAGCCCCCGCGGTGAATGGAGCCACTGGCCACAGCAGCAGTTTGGATG 300

Db 241 GGCACCTGGCGGATAGCCCCGCGGTGAATGGAGCCACTGGCCACAGCAGCAGTTTGGATG 300

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[illegible]

Db 301 CGCGGAGGTAATCCCCATGGCAGCAGTGAAGCAAGCGCTGAGAGAGGCTGGCGATGAGT 360

Qy 361 TTGAACTGCGGTACCGAGAGCATTCAGTGATCTAAACATCCAGCTTCATATATAACCCAG 420

100

[illegible]

421 GGACAGCATATCAGAGCTTTGAACACAGGTAGTGAACCTCTTTCCGGATGGGGTAAACT 480

421 GGACAGCATATCAGAGCTTTTGAACAGGTAGTGAAATGAACCTCTTTTCGGATGGGGTAAACT 480

[illegible]

481  
510

DB 481 GGGGTCGCATGTGGCCATCTCTCCCTTTGGCCGGGGCACCTGTGCGTGGAAAGCGTAGACA 540

541 AGGAGATGCAGGTATTGGTGAGTCGGATTGCAAGTTGGATGGCCACCTACCTGAATGACC 600

541 AGGAGATGCACGGTATTGGTGAGTCGGATTGCAAGTTGGATGGCCACCTACCTGCAATGACC 600

601 ACCTAGAGCCCTTGGATCCAGGAGAACCGCGGCTGGGACACTTTGTGGATCTCTACGGGA 660

QY 801 ACCATGAGGCCCTTGGATCCAGGAGGATCGCGGCTGGGACACTTTTGTGGATCTCTACGGGA 880

DB 601 ACC TAGAGCC TTGGA TC CAGGAGAA CCGCGGCTGGGACAC TT TGTGGATCTCTACGGGA 660

661 ACAATGCAGCCGAGAGCCGGAAGGCCAGGAGCGTTTCAACCGCTGGTTCTTGACGG 720

## RESULT 2

RESOLUTION  
ADE85177

ID ADE85177 standard; DNA; 1466 BP.

AC ADE85177:

XX  
XX  
RECORDS

DT 29-JAN-2004 (first entry)

XXXXXX

DE Farnesyl transferase inhibitor modulated leukemia associated gene #396.

XX

KW ss; cytostatic; farnesyl transferase inhibitor; gene expression;

KW quinolinone; leukemia; cancer.











601 ACCTAGAGCCTTGATTCAGGAGAAACGGCGCTGGGACACCTTTGTGTGATCTCTACGGGA 660  
1195  
896 ACCTAGAGCCTTGATTCAGGAGAAACGGCGCTGGGATACCTTTGTGTGAACTCTATGGGA 955  
1195  
661 ACAATGACAGCAGCCGAGAGCCGGAAGACCGAGGAGCGTTTCAACGCTGGTTCCTGACGG 720  
1195  
956 ACAATGACAGCAGCCGAGAGCCGGAAGGACCGAGGAGCGTTTCAACGCTGGTTCCTGACGG 1015  
1195  
721 GCATGACTGTGGCTGGTGTAGTTCTGTCTGGGCTCACTCTTCAGTCGGAAGTGACGACACA 780  
1195  
1016 GCATGACTGTGGCGGGGTGGTCTGTCTGGGCTCACTCTTCAGTCGGAATGACGACACA 1075  
1195  
781 CTGACCGTCCACTCACTCTCACTCTCCACCTTGCCTCCACACACAACTCTCTCTTCAGCC 840  
1195  
1076 CTGACCATCCACTCACTCTCCACCTTCCACCTTCTCTGTCTCCACACATCTCTCGTCCAGCC 1135  
1195  
841 ACCATTGCTACGAGAGAACCACTACATGCAACTCAGCCCTCTTCCCTATTTATAGGGTT 900  
1195  
1136 GCCATTGCCACGAGAGAACCACTACATGCAAGCCATGCCACCTGCCCATCACAGGGTT 1195  
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901 GGGCTAGACGAGTCCCTCGAGTGTAGTCTTCTAGATCTACCAAGCTTCTGTGGAAGC 960  
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1196 GGGCCAGATCTGGTCCCTCGAGTGTAGTCTTCTAGATTTATCACACTTCTGTGAGA- 1253  
1195  
961 CACCTTCCCCCAACATCTCAGTTCCTTGGCTCAAACTCACAAGTCTTCTCTCAGAT 1020  
1195  
1254 -----CCCCACACCTCAGTTCCTTGGCTCAGAAATTCACAA-AATTTCCACAAAT 1305  
1195  
1021 CAGCTCTCTTGGAGCTGGCAGAGTGGGAAGGGGTGTCTAGAGGG--AGAAGAGCCTGC 1078  
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1306 CTGTCCAAAGAGGCTGGCAGATGGAAGGGTGTGTGGCTGGGGCAGGAGGGCCCTAC 1365  
1195  
1079 CTGTGTGTGGAGCCCTGATTAACCTCAGCTCTCGGGAATGCTTCTTGGCAGGAGC 1138  
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1366 CTGATTGGTGAACCT--TACCCCTAGCCTCCTCGAAATGTTTTCTGCCAGGAGC 1423  
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1139 TGGAGAGCTCTTAAACCTCTTCCC-----CAGAGACTAGATTGCTTGGTGTGTGATGTG 1194  
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1424 TTGAAGTTTTCAGAACTCTTCCCAGAAAGGAGCTAGATTGCTTGTGTTGATGTT 1483  
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1195 TGTGGCTCAGAAATGATTCATTTCCCAATCTGTCTGTCTGCTGGGGCGGCTCCTCCTTC 1254  
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1484 TGTGGCTCAGAAATGATTCATTTTCCCTCCCACTCTCCCACTAACTGCGGTTCCTTT 1543  
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1255 CCATCTCCACCCCTCCCTCCAGAGCCATTTGAGTGTGCTTTGACCTTTTGACTA 1314  
1195  
1544 CC--TTCCATCCCTACCCCTAAGAGCCATTTAGGGGCACTTT-----TG 1587  
1195  
1315 ACTAAATGACGCTGTGGGATAACGAGGCAAGGACCT-----CCTCCCACTGT 1368  
1195  
1588 ACTAGGATTCAGGCTGTGGGATAAAGATGCAAGGACGAGCTCCTCTCCTCCTCT 1647  
1195  
1369 GGCCTGGCCA-AGCCCTCCTCTGCTGTGATGTTCTCTGAGGCTCTCTGCTAGAGTC 1427  
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1648 GGCCTGCTAGAGTCTCTCACTCCCACTGCTCAAAATGCTCTCCAGAGGCTCTGCTAGAGC 1707  
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1428 CAGCCCAACCAAGAG--GAGGAGCGAGCTGCGGAAGTCCACCTTCGAGAGCCTGA 1484  
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1708 CAGCCCAACCAAGAGGAGGGGCTATAGCTACAGGAAGCACCCTACGCAAAAGCTAGG 1767  
1195  
1485 GCGGCTCTTGGGCTTAGCACACCCAGATCTCTTCCACCTCCCTCCCTGCTCATGG 1544  
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1768 GTGGCCCTTGCAATTCAGACACCTTAGTCTCTTCCCTCTCTGCTC-----CC 1818  
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1545 TGACCATGACTGAGGACCAATGCGGCCCAAGCTAGAGTGGCCAGAGCTGTTAATGACTT 1604  
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1819 ATGACCATGAGGACCAATGCGGCCCAAGCAGATGCTGCTGTTATGGCT 1878  
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1605 CAGCTGCTCTCTCTGCAAGATCAGCTGTGGATCTTTCCTTGGTGTGCTGCGCA 1664  
1195  
1879 CAGCTGCTCTCTCTCTAAGAGAGCAGCTGTGGATCTTTCCTTGGG-----CTGCTCT 1935  
1195  
1665 GGGTCCAGGAGCTCTGGCTTAGCCCAAGTGTGAGGAAGCTTACA-GCGCAGCTATGG 1723  
1195

Db 1936 CATGTTGGTTCAGGGGACTCAGCCCTGAGTGAAGGAGCTATCAGGAACAGCTATGG 1995  
Qy 1724 GAGCCCTGGGGCTTCCCT 1742  
Db 1996 GAGCCCAAGGCTCTTCCCT 2014  
RESULT 5  
ADP54991  
ID ADP54991 standard; cDNA; 2575 BP.  
XX AC ADP54991;  
XX 18-NOV-2004 (first entry)  
XX Human PRO cDNA sequence SEQ ID NO:967.  
XX human; PRO; immune related disease; inflammatory immune response;  
XX immune response stimulation; antiallergic; antianaemic; antiarthritic;  
XX antiasthmatic; antidiabetic; antinflammatory; antipsoriatic;  
XX ancinematoc; antithyroid; CNS; dermatological; gastrointestinal;  
XX haemostatic; hepatotropic; immunostimulant; immunosuppressive; muscular;  
XX nephrotropic; neuroprotective; osteopathic; respiratory; vasotropic;  
XX virucide; gene therapy; gene; ss.  
XX Homo sapiens.  
XX WO2004039956-A2.  
XX 13-MAY-2004.  
XX 28-OCT-2003; 2003WO-US034381.  
XX 29-OCT-2002; 2002US-0422472P.  
XX (GETH ) GENENTECH INC.  
XX Aggarwal S, Clark H, Gurney AL, Schoenfeld J, Williams PM;  
XX Wood WI, Wu TD;  
XX WPI; 2004-376182/35.  
XX P-PSDB; ADP54992.  
XX New PRO polynucleotides and polypeptides, useful in useful in diagnosing  
XX and treating an immune related disease, e.g. systemic lupus  
XX erythematosus, rheumatoid arthritis, diabetes mellitus or asthma and in  
XX stimulating an immune response.  
XX Claim 2; SEQ ID NO 967; 3009pp; English.  
XX The present invention describes an isolated PRO nucleic acid (1). Also  
XX described: (1) a vector comprising (1); (2) a host cell comprising the  
XX vector of (1); (3) a process for producing a PRO polypeptides; (4) an  
XX isolated PRO polypeptide; (5) a chimeric molecule comprising the  
XX polypeptide of (4) fused to a heterologous amino acid sequence; (6) an  
XX antibody which specifically binds to a polypeptide of (4); (7) a  
XX composition of matter comprising a polypeptide of (4), an agonist or  
XX antagonist of the polypeptide or an antibody that binds to the  
XX polypeptide in combination with a carrier; (8) an article of manufacture  
XX comprising a container, a label on the container and a composition of  
XX matter of (7); (9) a method of treating an immune related disease in a  
XX mammal; (10) a method for determining the presence of a PRO polypeptide  
XX in a sample suspected of having the polypeptide; (11) a method of  
XX diagnosing an immune related disease or an inflammatory immune response  
XX in mammal; (12) a method of identifying a compound that inhibits or  
XX mimics the activity of or expression of a gene encoding a PRO polypeptide  
XX ; and (13) a method of stimulating the immune response in a mammal. The  
XX PRO sequences have antiallergic, antianaemic, antiarthritic,  
XX antiasthmatic, antidiabetic, antinflammatory, antipsoriatic,  
XX ancinematoc, antithyroid, CNS, dermatological, gastrointestinal,  
XX haemostatic, hepatotropic, immunostimulant, immunosuppressive, muscular,  
XX nephrotropic, neuroprotective, osteopathic, respiratory, vasotropic and







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QY 961 CACCTTCCCCACATCTCAGTTCCTTGGCTCAAAACTCAGAAGTTTTTCTCAGAT 1020
Db 1287 -----CCCCACACCTCAGTTCCTTGGCTCAGAATTCACAA-ANTTCCAAAAAT 1338
QY 1021 CAGCTCCTTGGAGGTGCGCAGAGTGGGAAGGGGTGTCTAGAGG--AGAAGAGCCTGC 1078
Db 1339 CTGTCCAAAGAGGCTGCGCAGGTATGGAAGGTTTGTGGCTGGGCGCAGGAGGCCCTAC 1398
QY 1079 CTTGTGTGGGACCTGATTAACCTTGAGCTCTCGGAATGCTTTTCTGGCAGGAGC 1138
Db 1399 CTGATGTGTGCAACCT--TACCCCTTAGCCTCCCTGAAAAATGTTTTCTGCCAGGAGC 1456
QY 1139 TGGAGAGCTCTCTAAACCTCTTCCCC---CAGAGACTAGATTGCTTGGTTTGTAGTG 1194
Db 1457 TTGAAGTTTTCAGAACCTCTTCCCGAAGAGGAGACTAGATTGCTTTGTTTTGTAGT 1516
QY 1195 TGTGGCCTCAGAAATGATFCCATTTCCCATTTCTGTGTCTCCCTGGGGGGCTCCTCCTTC 1254
Db 1517 TGTGGCCTCAGAAATGATCAATTTTCCCGCCCACTCTCCCACTAACTGAGGTTCCTTT 1576
QY 1255 CCATCTCACCCCGCCCGCCAGAGCCATTGAGTGAGGTCTTTTGGCCCTTTTGACTA 1314
Db 1577 CC--TTCCATCCTACCCCTTAAGAGCCATTTAGGGGCCACTTT-----TG 1620
QY 1315 ACTAAATGAGGCTGCTTGGGATACGAGGCAAGGACCT-----CCTCCCGACCTGT 1368
Db 1621 ACTAGGATTCAGGCTGCTTGGGATTAAGATGCAAGGACAGGACTCCTCTCACCTCT 1680
QY 1369 GGCCTGGCCA-AGCCCGCCACTCCTGTGTGAATGTTCTCTGAGGCCTCTGGCTAGAGTC 1427
Db 1681 GGACTGGCTAGAGTCTCACTCCCGAGTCCAAATGTCTCTCCAGAGCCCTCTGGCTAGAGC 1740
QY 1428 CAGCCCGCCAGAG---GAGGGACGAGCTGCGGAAAGTCCACCTTCGAGAGCCTGA 1484
Db 1741 CAGCCCGCCAGAGGAGGGGGCTATAGCTACAGGAAGCACCCCATGCTCCAAAGCTAGG 1800
QY 1485 GCGGCTCTGGGCTTAGCACACCCAGATCCTTCTCCACCCCTCCCTGGCTCCATGG 1544
Db 1801 GTGGCCCTTGAGGTTCAGACACACCTAGTCTCCCTTCCCTTGGCTC-----CC 1851
QY 1545 TGACCATGACTGAGGACCAACTGGGCGCCAGCTAGGTGCCCCAGAGCTGTTAATGACTT 1604
Db 1852 ATGACCATGACTGAGGACCAACTGGGCGCCAGACAGATGCCCCAGAGCTGTTATGGCT 1911
QY 1605 CAGTGCCTCACTTCTCTCAAGATCAGCCTGTGGCACTTTTGCCCTTGGGTGCTGCCACA 1664
Db 1912 CAGTGCCTCACTTCTCTCAAGAGCAGCCTGTGGCATCTTTGGCTTGGG---CTGCTCCT 1968
QY 1665 GGGTCCAGGACTCTGGCCTTAGCCCAAGCTGAGAGGAAGCTTACA-GCCGAGCTATGG 1723
Db 1969 CATGTGGTTTACGGGAGCTCAGCCCTGAGGTGAAAGGAGCTATCAGAAACAGCTATGG 2028
QY 1724 GAGCCCTGGGGCTTCCCT 1742
Db 2029 GAGCCCGAGGGTCTTCCCT 2047
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RESULT 8

```
ADQ97761
ID ADQ97761 standard; DNA; 71594 BP.
XX
AC ADQ97761;
XX
DT 07-OCT-2004 (first entry)
XX
DE Mouse cancer associated sequence MD10-042, SEQ ID 738.
XX
KW Cytostatic; Gene Therapy; cancer; leukemia; lymphoma; Mouse; ds.
XX
OS Mus musculus.
XX
PN WO2004060304-A2.

XX 22-JUL-2004.
XX
XX 22-DEC-2003; 2003WO-US041389.
XX
XX 27-DEC-2002; 2002US-00330773.
XX
XX (SAGR-) SAGRES DISCOVERY INC.
XX
XX Morris DW, Malandro MS;
XX
XX WPI; 2004-543781/52.
XX
XX New isolated cancer associated nucleic acids comprising at least 10
XX contiguous nucleotides; useful for diagnosing, preventing and/or treating
XX cancers such as leukemia and lymphoma.
XX
XX Claim 1; SEQ ID NO 738; 199pp; English.
XX
XX The present invention relates to cancer associated sequences (ADQ97025-
XX ADQ98004). The sequences are useful for the diagnosis, prevention and/or
XX treatment of cancer, such as leukemia and lymphoma. Note: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 71594 BP; 18772 A; 16295 C; 16965 G; 19461 T; 0 U; 101 Other;
XX
XX Query Match 46.6%; Score 811.6; DB 12; Length 71594;
XX Best Local Similarity 88.7%; Pred. No. 2e-222;
XX Matches 992; Conservative 0; Mismatches 89; Indels 37; Gaps 9;
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Db 5986 TAGGACACTTTTGTGGATCTCTACGGAAACATCAGCAGCGGAGCGGAAAGGCCAG 60045
QY 693 GAGCGTTTCAACCGCTGTTCTCAGCGGCATGACTGTGGCTGTGTGTGTCTGTCTGGC 752
Db 6046 GAGCGTTTCAACCGCTGTTCTCAGCGGCATGACTGTGGCTGTGTGTGTCTGTCTGGC 60105
QY 753 TCACCTTTCAGTGGGAAGTGACACGACTGACCGTCCACTCCTCCTCCTCCTCCTCCT 812
Db 60106 TCACCTTTCAGTGGGAAGTGACACGACTGACCGTCCACTCCTCCTCCTCCTCCTCCT 60165
QY 813 TGCCCCACACAACTCTCTTTCAGCGCAATGTCTACGAGGAGAACCTACATGCAA 872
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QY 873 CTCACGCCCCCTTCCCTTATATAGGGTTGGGCTTAGACGGAGTCCCTGCAAGTTAGCTTT 932
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QY 933 CTAGAATCTACACGCTTCTGTGAAAGCCACTTTCCCGCCCAATCTCAGTTTCCCTTGCC 992
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Db 60406 GGTGTG--TGAGGAGGAGAGCGCTGCTGTGTGGGACCTGATTAACCTCCTGAGCCTC 60463
QY 1113 TCGGGAATGCTTTTCTGGCAGGAGCTGGAGAGCTCTCTAAACCTCTTCTCCCGCAGAGACT 1172
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	Qy	1352	----ACCCTCTGCCACCTGTGGCTGTGGCC--AAGCCCCCATCTCCTGTCTGTAATGTCTCT	1405
	Db	60680	CCAGAAGCTCTCTCCCACTGTGGCCGTGGCCAACCCCCACTTTGTGTCTGAATGTCTCT	60739
	Qy	1406	CCTGAGGCCCTCTGGCTAGAGTCCAGGCCACACCAGAGGAGGAGCGGAGCTCGCGAAAAGT	1465
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	Qy	1706	CT-TACAGCCGACTATGGAGCCCTGGGGGCTTCCTT	1742
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## RESULT 9

ADH52632	
ID	ADH52632 standard; DNA; 863 BP.
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AC	ADH52632;
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DT	25-MAR-2004 (first entry)
XX	
DE	Chinese hamster anti-apoptosis bcl-xL wild-type DNA.
XX	
KW	mammalian myeloma host cell; protein production; anti-apoptosis;
XX	cell death; Chinese hamster; bcl-xL; wild-type; ds; gene.
OS	Cricetulus griseus.
XX	
PN	US2003219871-A1.
XX	
PD	27-NOV-2003.
XX	
PF	28-MAR-2003; 2003US-00402017.
XX	
PR	02-APR-2002; 2002US-0369307P.
XX	
PA	(BOEH ) BOEHRINGER INGELHEIM PHARMA GMBH & CO KG.
XX	
PI	Enenkel B, Meents H, Fussenegger M;
XX	
DR	WPI; 2004-033642/03.
DR	P-PSDB; ADH52633.
XX	
PT	New genetically engineered hamster or murine myeloma host cells
PT	comprising enhanced levels of active anti-apoptosis genes, useful for
PT	producing complex protein therapeutics.
XX	
PS	Claim 57; SEQ ID NO 3; 46pp; English.
XX	
CC	The invention relates to a novel mammalian host cell for producing

CC	protein therapeutics. The host cell comprises a hamster or a murine
CC	myeloma cell that is genetically modified by introduction of nucleic acid
CC	sequences encoding an anti-apoptosis gene, a selectable amplifiable
CC	marker gene and at least one gene of interest. The host cell of the
CC	invention may be useful for producing at least one protein encoded by a
CC	gene of interest. The DNA, polypeptide and the methods may be used for
CC	inhibiting or delaying cell death. The current sequence is that of the
CC	Chinese hamster anti-apoptosis bcl-xL wild-type DNA of the invention.
XX	
SQ	Sequence 863 BP; 212 A; 227 C; 247 G; 177 T; 0 U; 0 Other;
	Query Match 45.2%; Score 787.8; DB 12; Length 863;
	Best Local Similarity 94.6%; Pred. No. 1.9e-216;
	Matches 816; Conservative 0; Mismatches 47; Indels 0; Gaps 0;
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Db	61 ATTATATAAATGTCTCAGAGCAACCGGGAGCTAGTGGTTGACTTCTCTCTCAAGATC 120
Qy	123 TCCCAGAAAGGATACAGCTGCAGTGCAGTGTAGCGATGCTCGAAGAGAACAGGACTGAGGCC 182
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Db	121 TCCCAGAAAGGATACAGCTGCAGTGTAGTGTAGTGTGGAAGAGAACAGGACTGAGGCC 180
Qy	183 CCAGAAAGAACTGAAACCAGAAAGGAGACCCCCAGTGCCTCATATGGCAACCCATCCTGG 242
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Qy	243 CACTGGCGGATAGCCCCCGCGGTGAATGAGAGCCA CTGGCCACAAGCAGAGCTTTGGATGCG 302
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Db	241 CACTGGCGGACAGCCCCCGGTGAATGAGAGCCACTGGCCACAAGCAGAGCTTTGGATGCA 300
Qy	303 CGGGAGGTATCCCCATGGCAGCAGGTGAAGCAGCGCTGAGAGAGCTGCGGATGAGTTT 362
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Qy	363 GAATCGCGGTACCGGAGAGCATTTCACTGATCTAAACATCCCAGCTTCATATAACCCACAGG 422
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Qy	423 ACAGCATATCAGAGCTTTGAAACAGGTAGTGAATGAATCTTTCCGGATGGGGTAAACTCG 482
Db	
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Qy	483 GGTCGCATTGTGGCTTCTTCTCTTTGGCGGGGCACTGTGCGTGAAGAAGCGTAGACAAG 542
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Qy	783 GACCGTCCACTCACCTCTCACCTCCACCTTGCCCCCACCACCAACTCTCTCTTCAGCCAC 842
Db	
Db	781 GACCACTACTCACTCGCTCTCCACCCTATCCCCACCAACTCTCTCTTCAGCCAC 840
Qy	843 CATTTGCTACAGGAGAACCACTA 865













[illegible]

Search completed: March 31, 2005, 00:50:27  
Job time : 924 secs

100

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: March 31, 2005, 00:32:47 ; Search time 322 Seconds  
(without alignments)  
8852.155 Million cell updates/sec

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Perfect score: 1742  
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Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA.\*  
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2: /cgn2\_6/ptodata/1/ina/5B COMB.seq.\*  
3: /cgn2\_6/ptodata/1/ina/6A COMB.seq.\*  
4: /cgn2\_6/ptodata/1/ina/6B COMB.seq.\*  
5: /cgn2\_6/ptodata/1/ina/PTCUS COMB.seq.\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	741	42.5	926	3	US-08-481-739-1
2	741	42.5	926	5	PCT-US94-07089-6
3	737.8	42.4	926	1	US-08-081-448-5
4	737.8	42.4	926	2	US-08-470-670A-6
5	737.8	42.4	926	3	US-09-167-921-1
6	737.8	42.4	926	3	US-09-277-020-39
7	737.8	42.4	926	3	US-09-323-743-1
8	737.8	42.4	926	3	US-08-461-511A-6
9	737.8	42.4	926	4	US-09-023-655-1430
10	737.8	42.4	926	4	US-09-814-915A-106
11	736.2	42.3	926	3	US-09-271-014A-5
12	627.6	36.0	1236	4	US-09-639-245-1
13	599.2	34.4	1384	4	US-08-899-367-1
14	576.8	33.1	60489	4	US-09-949-016-16287
15	563	32.3	1455	4	US-09-639-245-7
16	399	22.9	737	4	US-09-949-016-4545
17	399	22.9	737	4	US-09-023-655-1458
18	399	22.9	737	5	PCT-US94-07089-8
19	395.8	22.7	737	1	US-08-081-448-7
20	395.8	22.7	737	2	US-08-470-670A-8
21	395.8	22.7	737	3	US-08-461-511A-8
22	395.8	22.7	737	3	US-09-271-014A-7
23	338.4	19.4	1274	2	US-08-470-670A-1
24	338.4	19.4	1274	3	US-08-461-511A-1
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27	338.4	19.4	1303	3	US-09-271-014A-1

28	155.2	8.9	717	2	US-08-465-485A-20	Sequence 20, Appl
29	155.2	8.9	717	3	US-09-080-285-20	Sequence 20, Appl
30	155.2	8.9	4825	6	5459251-1	Patent No. 5459251
31	155.2	8.9	4825	6	5459251-1	Patent No. 5459251
32	155.2	8.9	5086	2	US-08-465-485A-19	Sequence 19, Appl
33	155.2	8.9	5086	2	US-08-365-486A-14	Sequence 14, Appl
34	155.2	8.9	5086	3	US-09-080-285-19	Sequence 19, Appl
35	155.2	8.9	5086	3	US-08-880-342-14	Sequence 14, Appl
36	155.2	8.9	5086	3	US-09-724-426-19	Sequence 19, Appl
37	155.2	8.9	5086	3	US-09-233-527-7	Sequence 7, Appl
38	155.2	8.9	5086	5	PCT-US93-05651-4	Sequence 4, Appl
39	155.2	8.9	5086	5	PCT-US93-06251-2	Sequence 2, Appl
40	155.2	8.9	5094	3	US-09-234-186-7	Sequence 7, Appl
41	155.2	8.9	5104	6	5506344-1	Patent No. 5506344
42	155.2	8.9	5104	6	5506344-1	Patent No. 5506344
43	154.2	8.9	1846	2	US-08-365-486A-16	Sequence 16, Appl
44	154.2	8.9	1846	3	US-08-880-342-16	Sequence 16, Appl
45	154.2	8.9	6030	4	US-09-023-655-1015	Sequence 1015, Ap

ALIGNMENTS

RESULT 1  
US-08-481-739-1  
; Sequence 1, Application US/08481739  
; Patent No. 6143291  
; GENERAL INFORMATION:  
; APPLICANT: June, Carl H. and Thompson, Craig B.  
; TITLE OF INVENTION: METHODS FOR ENHANCING T CELL SURVIVAL  
; TITLE OF INVENTION: BY AUGMENTING BCL-XL PROTEIN LEVELS  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD  
; STREET: 28 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/481,739  
; FILING DATE: 07-JUNE-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/435,518  
; FILING DATE: 04-MAY-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: DeConti, Giulio A. (GAD)  
; REGISTRATION NUMBER: 31,503  
; REFERENCE/DOCKET NUMBER: RPI-034CP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)742-4214  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 926 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 135..836  
; US-08-481-739-1

Query Match 42.5%; Score 741; DB 3; Length 926;  
Best Local Similarity 91.3%; Pred. No. 1.2e-218;  
Matches 786; Conservative 0; Mismatches 75; Indels 0; Gaps 0;









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## RESULT 6

US-09-277-020-39  
; Sequence 39, Application US/09277020  
; Patent No. 6210892  
; GENERAL INFORMATION:  
; APPLICANT: Bennett, C. Frank  
; TITLE OF INVENTION: Alteration of Cellular Behavior by Antisense Modulation  
; FILE REFERENCE: ISPH-0339  
; CURRENT APPLICATION NUMBER: US/09/277,020  
; CURRENT FILING DATE: 1999-03-26  
; EARLIER APPLICATION NUMBER: 09/167,921  
; EARLIER FILING DATE: 1998-10-07  
; NUMBER OF SEQ ID NOS: 65  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 39  
; LENGTH: 926  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-277-020-39

Query Match 42.4%; Score 737.8; DB 3; Length 926;  
Best Local Similarity 91.1%; Pred. No. 1.2e-217;  
Matches 784; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

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Db |||||  
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Qy 841 ACCATTGCTACAGGAGAAC 861  
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904 GCCATTGCCACAGGAGAAC 924

## RESULT 7

US-09-323-743-1  
; Sequence 1, Application US/09323743  
; Patent No. 6214986  
; GENERAL INFORMATION:  
; APPLICANT: Bennett, C. Frank  
; APPLICANT: Dean, Nicholas M.  
; APPLICANT: Monia, Brett P.  
; APPLICANT: Nickoloff, Brian J.  
; APPLICANT: Zhang, Qingqing  
; TITLE OF INVENTION: Antisense Modulation of bcl-x Expression

5









APPLICATION NUMBER: US/08/899,367  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Amy E. Mandragouras  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: DEN-019  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)227-5941  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1384 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 378..1085  
US-08-899-367-1

Query Match 34.4%; Score 599.2; DB 4; Length 1384;  
Best Local Similarity 96.4%; Pred. No. 1.2e-174;  
Matches 613; Conservative 0; Mismatches 23; Indels 0; Gaps 0;  
Qy 1 CACGAGCAGACCCAGTGAAGTGAAGTGTGTTGGACAATGGACTGGTGGAGCCCATCT 60  
Db 307 CACGAGCAGACCCAGTGAAGTGAAGTGTGTTGGACAATGGACTGGTGGAGCCCATCT 366  
Qy 61 CTATTATAAATGTCTCAGAGCACCGGAGCTGGTGTGACTTTCTCTCTACAGC 120  
Db 367 CTATTATAAATGTCTCAGAGCACCGGAGCTGGTGTGACTTTCTCTCTACAGC 426  
Qy 121 TCTCCAGAAAGGATACAGCTGGAGTCAAGTGTGCGATGTGCGAAGAACAGGACTGAAG 180  
Db 427 TTTCCAGAAAGGATACAGCTGGAGTCAAGTGTGCGATGTGCGAAGAACAGGACTGAAG 486  
Qy 181 CCCAGAAAGAACCTGAACCCAGAAAGGAGACCCCGAGTGCATCAATGGCAACCCATCCT 240  
Db 487 CCCAGAAAGAACCTGAACCCAGAAAGGAGACCCCGAGTGCATCAATGGCAACCCATCCT 546  
Qy 241 GGCACCTGGCGATAGCCCGCGTGAATGAGCCACTGGCCACAGCAGCAGTTTGGATG 300  
Db 547 GGCACCTGGCGATAGCCCGCGTGAATGAGCCACTGGCCACAGCAGCAGTTTGGATG 606  
Qy 301 CGCGGAGGTAAATCCCATGGCAGCAGTGAAGCAAGCGCTGAGAGAGGCTGGCGATGAGT 360  
Db 607 CGCGGAGGTAAATCCCATGGCAGCAGTGAAGCAAGCGCTGAGAGAGGCGATGAGT 666  
Qy 361 TTGAATCGCGTACCGGAGAGCATTCAGTGAATCAATCAATCCAGCTTCATATAACCCAG 420  
Db 667 TTGAATCGCGTACCGGAGAGCATTCAGTGAATCAATCAATCCAGCTTCATATAACCCAG 726  
Qy 421 GGACAGCATATCAGAGCTTTGAAACAGGTAGTGAATGAATCTTTTCGGATGGGTTAACT 480  
Db 727 GGACCGCATATCAGAGCTTTGAAACAGGTAGTGAATGAATCTTTTCGGATGGGTTAACT 786  
Qy 481 GGGGTGCGATTTGGCCCTTTCTCTCTTTGGCGGGCACTGGCGTGGAAAGCGTAGACA 540  
Db 787 GGGGTGCGATTTGGCCCTTTCTCTCTTTGGCGGGCACTGGCGTGGAAAGCGTAGACA 846  
Qy 541 AGGAGATCAGGTATTTGGTGAAGTGGATTTGCAAGTTGGATGGCCACCTTACCTGAATGACC 600  
Db 847 AGGAGATCAGGTATTTGGTGAAGTGGATTTGCAAGTTGGATGGCCACCTTACCTGAATGACC 906  
Qy 601 ACCTAGAGCCTTGGATTCAGAGAACGGCGCTGGG 636  
Db 907 ACCTAGAGCCTTGGATTCAGAGAACGGCGCTGGG 942

## RESULT 14

US-09-949-016-16287  
Sequence 16287 Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: Fast-Seq for Windows Version 4.0  
SEQ ID NO 16287  
LENGTH: 60489  
TYPE: DNA  
ORGANISM: Human  
US-09-949-016-16287

Query Match 33.1%; Score 576.8; DB 4; Length 60489;  
Best Local Similarity 94.2%; Pred. No. 1.1e-166;  
Matches 599; Conservative 0; Mismatches 37; Indels 0; Gaps 0;  
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Db 2064 CACGAGCAGACTCAGTGAAGTGAAGTGTGTTGGACAATGGACTGGTGGAGCCCATCT 2123  
Qy 61 CTATTATAAATGTCTCAGAGCACCGGAGCTGGTGTGACTTTCTCTCTACAGC 120  
Db 2124 CTATTATAAATGTCTCAGAGCACCGGAGCTGGTGTGACTTTCTCTCTACAGC 2183  
Qy 121 TCTCCAGAAAGGATACAGCTGGAGTCAAGTGTGCGATGTGCGAAGAACAGGACTGAAG 180  
Db 2184 TTTCCAGAAAGGATACAGCTGGAGTCAAGTGTGCGAAGAACAGGACTGAAG 2243  
Qy 181 CCCAGAAAGAACCTGAACCCAGAAAGGAGACCCCGAGTGCATCAATGGCAACCCATCCT 240  
Db 2244 CCCAGAAAGGACTGAATCCGAGATGAGACCCCGAGTGCATCAATGGCAACCCATCCT 2303  
Qy 241 GGCACCTGGCGATAGCCCGCGTGAATGAGCCACTGGCCACAGCAGCAGTTTGGATG 300  
Db 2304 GGCACCTGGCGAGACAGCCCGCGTGAATGAGCCACTGGCCACAGCAGCAGTTTGGATG 2363  
Qy 301 CGCGGAGGTAAATCCCATGGCAGCAGTGAAGCAAGCGCTGAGAGAGGCTGGCGATGAGT 360  
Db 2364 CCCGGAGGTGAATCCCATGGCAGCAGTGAAGCAAGCGCTGAGAGAGGCGATGAGT 2423  
Qy 361 TTGAATCGCGTACCGGAGAGCATTCAGTGAATCAATCAATCCAGCTTCATATAACCCAG 420  
Db 2424 TTGAATCGCGTACCGGAGAGCATTCAGTGAATCAATCAATCCAGCTTCATATAACCCAG 2483  
Qy 421 GGACAGCATATCAGAGCTTTGAAACAGGTAGTGAATGAATCTTTTCGGATGGGTTAACT 480  
Db 2484 GGACAGCATATCAGAGCTTTGAAACAGGTAGTGAATGAATCTTTTCGGATGGGTTAACT 2543  
Qy 481 GGGGTGCGATTTGGCCCTTTCTCTCTTTGGCGGGCACTGGCGTGGAAAGCGTAGACA 540  
Db 2544 GGGGTGCGATTTGGCCCTTTCTCTCTTTGGCGGGCACTGGCGTGGAAAGCGTAGACA 2603  
Qy 541 AGGAGATCAGGTATTTGGTGAAGTGGATTTGCAAGTTGGATGGCCACCTTACCTGAATGACC 600  
Db 2604 AGGAGATCAGGTATTTGGTGAAGTGGATTTGCAAGTTGGATGGCCACCTTACCTGAATGACC 2663  
Qy 601 ACCTAGAGCCTTGGATTCAGAGAACGGCGCTGGG 636  
Db 2664 ACCTAGAGCCTTGGATTCAGAGAACGGCGCTGGG 2699



## RESULT 15

US-09-639-245-7  
; Sequence 7, Application US/09639245  
; Patent No. 6737511  
; GENERAL INFORMATION:  
; APPLICANT: Youle et al.  
; TITLE OF INVENTION: RECEPTOR-MEDIATED UPTAKE OF AN EXTRACELLULAR BCL-XL  
; FILE REFERENCE: 4239-55417  
; CURRENT APPLICATION NUMBER: US/09/639,245  
; CURRENT FILING DATE: 2000-08-15  
; PRIOR APPLICATION NUMBER: 60/149,220  
; PRIOR FILING DATE: 1999-08-16  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 7  
; LENGTH: 1455  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: genetic fusion  
; NAME/KEY: CDS  
; LOCATION: (1)..(1455)  
US-09-639-245-7

Query Match 32.3%; Score 563; DB 4; Length 1455;

Best Local Similarity 92.9%; Pred. NO. 2e-163;

Matches 590; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

Qy	63	ATTATAAATGCTCTCAGAGCAACCGGAGCTGGTGGTGTGACTTCTCTCTACAGCTC	122
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Qy	123	TCCAGAAAGGATACAGCTGGAGTCAGTTTAGCGATGTGGAAGAGAACAGGACTGAAGCC	182
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Qy	183	CCAGAAGAACTGAACCCAGAAAGGAGACCCCGAGTGCATCAATGGCAACCCATCTGG	242
Db	940	CCAGAAGGACTGAATCGGAGATGGAGACCCCGAGTGCATCAATGGCAACCCATCTGG	999
Qy	243	CACCTGGGGATAGCCCGCGGTGAATGGAGCCACTGGCCACAGCAGAGTTTGGATGCG	302
Db	1000	CACCTGGCAGACACCCCGCGGTGAATGGAGCCACTGGCCACAGCAGAGTTTGGATGCG	1059
Qy	303	CGGAGGTTAATCCCATGCGCAGCAGTGAAGCAAGCGCTGAGAGAGGCTGGCGATGAGTTT	362
Db	1060	CGGAGGTTAATCCCATGCGCAGCAGTGAAGCAAGCGCTGAGAGAGGCTGGCGATGAGTTT	1119
Qy	363	GAACTGGCGTACCAGAGACATTCAGTGATCTAACATCCAGCTTTCATATAACCCAGGG	422
Db	1120	GAACTGGCGTACCAGAGACATTCAGTGATCTAACATCCAGCTTTCATATAACCCAGGG	1179
Qy	423	ACAGCATATCAGAGCTTTGAACAGGTAGTGAATGAATCTTTTCGGGATGGGGTAACTGG	482
Db	1180	ACAGCATATCAGAGCTTTGAACAGGTAGTGAATGAATCTTTTCGGGATGGGGTAACTGG	1239
Qy	483	GGTGGCATTTGGGCTTTCTCTCTTTGGCGGGCAGTGGCTGGGAAGGCTAGACAAG	542
Db	1240	GGTGGCATTTGGGCTTTCTCTCTTTGGCGGGCAGTGGCTGGGAAGGCTAGACAAG	1299
Qy	543	GAGATGCAGGTATTGGTGGATTCGAATTCGAATTCGATGGCCACCTCAATGAATGACCA	602
Db	1300	GAGATGCAGGTATTGGTGGATTCGAATTCGAATTCGATGGCCACCTCAATGAATGACCA	1359
Qy	603	CTAGAGCTTGGATCCAGAGAAACCGCGGTGGGACACTTTTGTGGATCTCTACGGGAAC	662
Db	1360	CTAGAGCTTGGATCCAGAGAAACCGCGGTGGGACACTTTTGTGGATCTCTACGGGAAC	1419
Qy	663	AATGCAGCAGCCGAGAGCCGAAAGGCCAGAGCG	697
Db	1420	AATGCAGCAGCCGAGAGCCGAAAGGCCAGAGCG	1454

Search completed: March 31, 2005, 04:26:50  
Job time : 325 secs

THE COGNATE

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: March 31, 2005, 00:35:02 ; Search time 6357 Seconds  
(without alignments)  
1658.556 Million cell updates/sec

Title: US-10-049-822A-1

Perfect score: 1742

Sequence: 1 cacagagcagaccagtgag.....ggagccctggggcttcct 1742

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5607317 seqs, 3026245999 residues

Total number of hits satisfying chosen parameters: 11214634

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:\*

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- 2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*
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- 5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*
- 6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq:\*
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- 9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:\*
- 10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*
- 12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*
- 13: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:\*
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- 15: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*
- 16: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq:\*
- 17: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq:\*
- 18: /cgn2\_6/ptodata/1/pubpna/US10F\_PUBCOMB.seq:\*
- 19: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*
- 20: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq:\*
- 21: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*
- 22: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1168	67.0	1466	18 US-10-283-975A-394	Sequence 394, App
2	787.8	45.2	863	17 US-10-402-017-3	Sequence 3, Appli
3	737.8	42.4	926	9 US-09-734-846-1	Sequence 1, Appli
4	737.8	42.4	926	9 US-09-734-846-1	Sequence 39, Appli
5	737.8	42.4	926	9 US-09-952-278-5	Sequence 5, Appli
6	737.8	42.4	926	15 US-10-072-830-3	Sequence 3, Appli
7	737.8	42.4	926	16 US-10-302-262-1	Sequence 1, Appli
8	737.8	42.4	926	17 US-10-402-017-1	Sequence 1, Appli
9	737.8	42.4	926	17 US-10-641-843-1430	Sequence 1430, Ap
10	737.8	42.4	926	18 US-10-717-597-87	Sequence 87, Appl
11	737.8	42.4	926	18 US-10-776-827-106	Sequence 106, App

12	737.8	42.4	926	18	US-10-825-282-47	Sequence 47, Appl
13	737.8	42.4	926	19	US-10-479-832A-3	Sequence 3, Appli
14	661.4	38.0	2386	17	US-10-388-360-351	Sequence 351, App
15	636	36.5	1748	17	US-10-388-934-539	Sequence 539, App
16	636	36.5	1748	17	US-10-191-803-202	Sequence 202, App
17	630	36.2	702	10	US-09-959-987-9	Sequence 9, Appli
18	627.6	36.0	1236	18	US-10-792-517-1	Sequence 1, Appli
19	599.2	34.4	1384	14	US-10-208-155-1	Sequence 1, Appli
20	563	32.3	1455	18	US-10-792-517-7	Sequence 13, Appli
21	560.2	32.2	636	16	US-10-169-223-13	Sequence 11, Appli
22	542.4	31.0	660	17	US-10-402-017-11	Sequence 9, Appli
23	540.8	31.0	660	17	US-10-402-017-9	Sequence 9, Appli
24	529.2	30.4	600	9	US-09-864-761-7360	Sequence 7360, Ap
25	528.8	29.4	564	16	US-10-029-386-20790	Sequence 20790, A
26	503.8	28.9	555	9	US-09-864-761-24081	Sequence 24081, A
27	425.6	24.4	600	17	US-10-402-017-7	Sequence 7, Appli
28	411.4	23.6	540	17	US-10-402-017-5	Sequence 5, Appli
29	399	22.9	737	17	US-10-641-643-1458	Sequence 1458, Ap
30	395.8	22.7	737	9	US-09-952-278-7	Sequence 7, Appli
31	390.6	22.4	492	10	US-09-918-995-33305	Sequence 33305, A
32	338.2	22.4	6509	15	US-10-311-455-199	Sequence 199, App
33	338.4	19.4	1303	9	US-09-952-278-1	Sequence 1, Appli
34	324.2	18.6	6509	15	US-10-311-455-200	Sequence 200, App
35	278.4	16.0	587	9	US-09-864-761-6802	Sequence 6802, App
36	278.4	16.0	587	16	US-10-029-386-3764	Sequence 3764, Ap
37	206	11.8	559	16	US-10-029-386-7084	Sequence 7084, Ap
38	191.8	11.0	378	10	US-09-918-995-34545	Sequence 34545, A
39	172.4	9.9	472	10	US-09-918-995-32037	Sequence 32037, A
40	170.6	9.8	476	10	US-09-918-995-267	Sequence 267, App
41	155.2	8.9	717	16	US-10-053-645A-20	Sequence 20, Appli
42	155.2	8.9	720	17	US-10-148-953A-6	Sequence 6, Appli
43	155.2	8.9	720	17	US-10-148-953A-8	Sequence 8, Appli
44	155.2	8.9	720	17	US-10-297-321-1	Sequence 1, Appli
45	155.2	8.9	931	18	US-10-714-310-18	Sequence 18, Appli

## ALIGNMENTS

RESULT 1  
US-10-283-975A-394  
; Sequence 394, Application US/10283975A  
; Publication No. US20040110792A1  
; GENERAL INFORMATION:  
; APPLICANT: Ortho-Clinical Diagnostics, Inc.  
; TITLE OF INVENTION: Methods For Assessing and Treating Leukemia  
; FILE REFERENCE: CDS 293 PCT  
; CURRENT APPLICATION NUMBER: US/10/283,975A  
; CURRENT FILING DATE: 2002-10-30  
; PRIOR APPLICATION NUMBER: 60/340,938  
; PRIOR FILING DATE: 2001-10-30  
; PRIOR APPLICATION NUMBER: 60/338,997  
; PRIOR FILING DATE: 2001-10-30  
; PRIOR APPLICATION NUMBER: 60/340,081  
; PRIOR FILING DATE: 2001-10-30  
; PRIOR APPLICATION NUMBER: 60/341,012  
; PRIOR FILING DATE: 2001-10-30  
; NUMBER OF SEQ ID NOS: 900  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 394  
; LENGTH: 1466  
; TYPE: DNA  
; ORGANISM: HUMAN  
US-10-283-975A-394

Query Match 67.0%; Score 1168; DB 18; Length 1466;  
Best Local Similarity 91.0%; Pred. No. 0;  
Matches 1331; Conservative 0; Mismatches 95; Indels 36; Gaps 7;  
Qy 1 CACAGAGCAGACCAGTGAGTGAGCAGGTGTTTGGACAAATGGACTGTTGAGCCCATCT 60  
Db 32 CACAGAGCAGACCAGTGAGTGAGCAGGTGTTTGGACAAATGGACTGTTTGGAGCCCATCT 91

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Qy 181 CCCAGAGAACTGAAACAGAAAGGAGAGCCCGAGTGCCATCAATGGCAACCCATCCT 240
Db 212 CCCAGAGAACTGAAAGCAGAGAGGAGAGCCCGAGTGCCATCAATGGCAACCCATCCT 271
Qy 241 GGCACCTGCGGATAGCCCGCGTGAATGAGCCACTGGCCACAGCAGCAGTTTGGATG 300
Db 272 GGCACCTGCGGATAGCCCGCGTGAATGAGCCACTGGCCACAGCAGCAGTTTGGATG 331
Qy 301 CGCGGAGGTTAATCCCATGTCAGCAGTGAAGCAAGCGCTGAGAGAGCTGGCGATGAGT 360
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Qy 1433 CCACCCAGGAGGAGGAGCGGAG 1454
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RESULT 2
US-10-402-017-3
; Sequence 3, Application US/10402017
; Publication No. US20030219871A1
; GENERAL INFORMATION:
; APPLICANT: Barbara ENENKEL, Heiko MEENTS and Martin FUSSENEGGER
; TITLE OF INVENTION: Host cells having improved survival properties and methods to gen
; FILE REFERENCE: Case 1/1314
; CURRENT APPLICATION NUMBER: US/10/402,017
; PRIOR FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: US 60/369,307
; PRIOR APPLICATION NUMBER: April 2, 2002
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 863
; TYPE: DNA
; ORGANISM: Cricetulus griseus
US-10-402-017-3

Query Match 45.2%; Score 787.8; DB 17; Length 863;
Best Local Similarity 94.6%; Pred. No. 3.5e-237;
Matches 816; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

Qy 3 CAGAGCAGACCCAGTGTGAGCAGGCTGTTTGGACAATGGACTGTGAGCCCATCTCT 62
Db 1 CAGAGCAGACCCAGTGTGAGCAGGCTGTTTGGACAATGGACTGTGAGCCCATCTGT 60
Qy 63 ATTATAAAATGTCTCAGAGCAACCGGAGCTGGTGGTTGACTTTCTCTCTACAAGCTC 122
Db 61 ATTATAAAATGTCTCAGAGCAACCGGAGCTAGTGGTTGACTTTCTCTCTACAAGCTC 120
Qy 123 TCCAGAAAGGATACAGCTGGAGTCAGTTTAGCGATGTGGAAGAGAAACAGAGCTGAAGCC 182
Db 121 TCCAGAAAGGATACAGCTGGAGTCAGTTTAGTCATGTGATGTGGAAGAGAAACAGAGCTGAAGCC 180
Qy 183 CCAGAAAGAACTGAAACAGAAAGGAGACCCCGAGTGCCATCAATGGCAACCCATCCTGG 242
Db 181 CCAGAAAGAACTGAAATCAGAGAGGAGACCCCGAGTGCCATCAATGGCAACCCATCCTGG 240
Qy 243 CACCTGCGGATAGCCCGCGGCTCAATGGAGCCACTGGCCACAGCAGCAGTTTGGATCGG 302
Db 241 CACCTGCGGAGACCGCCCGGCTCAATGGAGCCACTGGCCACAGCAGCAGTTTGGATCGA 300
Qy 303 CGGAGGATTAATCCCATGCGCAGCAGTGAAGCAAGCGCTGAGAGAGGCTGGCGATGAGTTT 362
Db 301 CGGAGGATTAATCCCATGCGCAGCAGTGAAGCAAGCGCTGAGAGAGGCGCGGATGAGTTT 360
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QY 363 GAACCTGGTACCGGAGGCAATTCAGTGAATCTAAATCCAGCTTCAATATACCCAGGG 422  
DB 361 GAGCTGGGTACCGGCGGGCTTCAGTGAATCTAAATCCAGCTTCAATATACCCAGGG 420  
QY 423 ACAGCATATCAGAGCTTTGAACAGGTAGTGAATGAATCTTTTCGGGATGGGTAACTGG 482  
DB 421 ACTGCATATCAAGCTTTGAACAGGTAGTGAATGAATCTTTTCGGGATGGGTAACTGG 480  
QY 483 GGTCCCATTTGGGCTTTCTCTCTTTGGCGGGGCACTGTGCTGGAAAGCGTAGACAAG 542  
DB 481 GGTCCCATTTGGGCTTTCTCTCTTTGGGCGGGGCACTGTGCTGGAAAGCGTAGACAAG 540  
QY 543 GAGATGCAAGGTATTTGGTGAATGCGATTCGAATTTGGATGGGCACTTCAATGAATGACCA 602  
DB 541 GAGATGCAAGGTATTTGGTGAATGCGATTCGAATTTGGATGGGCACTTCAATGAATGACCA 600  
QY 603 CTAGAGCTTGGATTCAGAGGAAACCGGCGCTGGGACACTTTTGTGGATCTCTACGGGAAC 662  
DB 601 CTAGAGCTTGGATTCAGAGGAAACCGGCGCTGGGACACTTTTGTGGATCTCTACGGGAAC 660  
QY 663 AATGAGCAGCGGAGAGCGGAAAGGCGGAGAGCGTTTCAACCGCTGTTCTTCAACCGGCG 722  
DB 661 AATGAGCAGCGTGAAGCGGAAAGGCGGAGAGCGTTTCAACCGCTGTTCTTCAACCGGCG 720  
QY 723 ATGACTGTGGCTGTGTAGTTCTGCTGGGCTCACTTTCACTGCTGGAAGTGAACGACACT 782  
DB 721 ATGACTGTGGCTGTGTAGTTCTGCTGGGCTCACTTTCACTGCTGGAAGTGAACGACACT 780  
QY 783 GACCGTCCACTCACTTCACTTCCACTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCT 842  
DB 781 GACCGTCCACTCACTTCACTTCCACTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCT 840  
QY 843 CATTTGCTACCGAGGAGCACTTA 865  
DB 841 CATTTGCTACCGAGGAGCACTTA 863

## RESULT 3

US-09-734-846-1  
; Sequence 1, Application US/09734846  
; Patent No. US20010007025A1  
; GENERAL INFORMATION:  
; APPLICANT: Bennett, C. Frank  
; APPLICANT: Dean, Nicholas M.  
; APPLICANT: Monia, Brett P.  
; APPLICANT: Nickoloff, Brian J.  
; APPLICANT: Zhang, QingQing  
; TITLE OF INVENTION: Antisense Modulation of bcl-x Expression  
; FILE REFERENCE: ISPH-0528  
; CURRENT APPLICATION NUMBER: US/09/734,846  
; CURRENT FILING DATE: 2000-12-12  
; PRIOR APPLICATION NUMBER: 09/277,020  
; PRIOR FILING DATE: 1998-03-26  
; PRIOR APPLICATION NUMBER: 09/167,921  
; PRIOR FILING DATE: 1998-10-07  
; PRIOR APPLICATION NUMBER: 09/323,743  
; PRIOR FILING DATE: 1999-06-02  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 926  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (135)..(836)  
; DATABASE ACCESSION NUMBER: L20121 Genbank  
; DATABASE ENTRY DATE: 1994-07-26

## US-09-734-846-1

Query Match 42.4%; Score 737.8; DB 9; Length 926;  
Best Local Similarity 91.1%; Pred. No. 2e-221;  
Matches 784; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

QY 1 CACAGACGAGACCAGTGAAGTGAAGTGTGTTTGGACAATGGACTGGTTGAGGCCATCT 60  
DB 64 CAGAGACGAGACTCAGTGAAGTGAAGTGTGTTTGGACAATGGACTGGTTGAGGCCATCT 123  
QY 61 CTATTATAAATGCTCTCAGAGCAACCGGAGCTGTGTTGACTTCTCTCTCTCTCTCTCT 120  
DB 124 CTATTATAAATGCTCTCAGAGCAACCGGAGCTGTGTTGACTTCTCTCTCTCTCTCTCT 183  
QY 121 TCTCCCAAGAAAGGATACAGCTGAGTGTGTTTACCGATGTGCAAGAGAAACAGGACTGAAG 180  
DB 184 TTTCCCAAGAAAGGATACAGCTGAGTGTGTTTACCGATGTGCAAGAGAAACAGGACTGAAG 243  
QY 181 CCCCAAGAAACCTGAACCAAGAGGAGACCCCGAGTGCCTCAATGGCAACCCATCTCT 240  
DB 244 CCCCAAGAAAGGACTGAATTCGAGATGGAGACCCCGAGTGCCTCAATGGCAACCCATCTCT 303  
QY 241 GGCACCTGGCGGATAGCCCGCGTGAATGAGAGCCACTGGCCACAGCAGCAGTGTGGATG 300  
DB 304 GGCACCTGGCGGATAGCCCGCGTGAATGAGAGCCACTGGCCACAGCAGCAGTGTGGATG 363  
QY 301 CGCGGAGGTAAATCCCATGGCAGCAGTGAAGCAAGCGCTGAGAGAGCTGGCGATGAGT 360  
DB 364 CCCGGAGGTGATCCCATGGCAGCAGTGAAGCAAGCGCTGAGAGAGCTGGCGATGAGT 423  
QY 361 TTGAACCTGGGTACCGGAGAGCAATTCAGTGAATCTAAACATCCAGCTTCAATATAACCCAG 420  
DB 424 TTGAACCTGGGTACCGGAGAGCAATTCAGTGAATCTAAACATCCAGCTTCAATATAACCCAG 483  
QY 421 GGACAGCATATCAGAGCTTTGAACAGGTAGTGAATGAATCTTTTCGGGATGGGTAACT 480  
DB 484 GGACAGCATATCAGAGCTTTGAACAGGTAGTGAATGAATCTTTTCGGGATGGGTAACT 543  
QY 481 GGGGTGCGATTGTGGCTTTCTCTCTTTGGCGGGGCACTGTGGTGGAAAGCGTAGACA 540  
DB 544 GGGGTGCGATTGTGGCTTTCTCTCTTTGGCGGGGCACTGTGGTGGAAAGCGTAGACA 603  
QY 541 AGGAGATGCAAGGTATTTGGTGAAGTGGATTTGCAAGTGGATGGCACTTACCTGAATGACC 600  
DB 604 AGGAGATGCAAGGTATTTGGTGAAGTGGATTTGCAAGTGGATGGCACTTACCTGAATGACC 663  
QY 601 ACCTAGAGCTTTGGATTCAGAGAGAACCGCGCTGGGACACTTTTGTGGATCTCTACGGGA 660  
DB 664 ACCTAGAGCTTTGGATTCAGAGAGAACCGCGCTGGGACACTTTTGTGGATCTCTACGGGA 723  
QY 661 ACAATGCAAGCAGCGAGAGCGGAAAGCCAGGAGCGTTTCAACCGCTGGTTCTTGACGG 720  
DB 724 ACAATGCAAGCAGCGAGAGCGGAAAGCCAGGAGCGTTTCAACCGCTGGTTCTTGACGG 783  
QY 721 GCATGACTGTGGCTGTGTAGTTCTTGTGGCTCACTCTTCAGTGGGAAGTGACAGACA 780  
DB 784 GCATGACTGTGGCTGTGTAGTTCTTGTGGCTCACTCTTCAGTGGGAATGACAGACA 843  
QY 781 CTGACCGTCCACTCACTTCACTTCCACTTCCACTTCCACTTCCACTTCTCTCTCTCTCT 840  
DB 844 CTGACCGTCCACTCACTTCACTTCCACTTCCACTTCCACTTCTCTCTCTCTCTCTCTCT 903  
QY 841 ACCATTGCTACCGAGGAGAAC 861  
DB 904 GCCATTGCCACCGAGGAGAAC 924

## RESULT 4

US-09-734-847A-39  
; Sequence 39, Application US/09734847A  
; Patent No. US20020049173A1  
; GENERAL INFORMATION:  
; APPLICANT: Bennett, C. Frank  
; APPLICANT: Crooke, Stanley T.  
; APPLICANT: Manoharan, Muthiah  
; APPLICANT: Wyatt, Jacqueline R.  
; APPLICANT: Baker, Brenda F.  
; APPLICANT: Monia, Brett P.





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/ ORGANISM: Homo sapiens
/
/ FEATURE:
/
/ NAME/KEY: CDS
/
/ LOCATION: (135)..(836)
/
/ DATABASE accession NUMBER: L20121 Genbank
/
/ DATABASE ENTRY DATE: 1994-07-26
US-10-302-262-1

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; TITLE OF INVENTION: Such Cells
; FILE REFERENCE: Case 1/1314
; CURRENT APPLICATION NUMBER: US/10/402.017
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: US 60/369,307
; PRIOR APPLICATION NUMBER: April 2, 2002
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 926
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-402-017-1

Query Match          42.4%; Score 737.8; DB 17; Length 926;
Best Local Similarity 91.1%; Pred. No. 2e-221;
Matches 784; Conservative 0; Mismatches 77; Indels 0; Gaps 0

Qy 1 CACAGACGACCCAGTCAGTCAGCAGGTGTTTTGGACAAATGAGCTGGTTGAGCCCATCT 60
Db 64 CAGAGACGAGACTCAGTCAGTCAGCAGGTGTTTTGGACAAATGAGCTGGTTGAGCCCATCT 123
Qy 61 CTATTATAAAAATGCTCAGAGCAACCGGAGCTGGTGGTTGACTTTCTCTCTCAACAAGC 120
Db 124 CTATTATAAAAATGCTCAGAGCAACCGGAGCTGGTGGTTGACTTTCTCTCTCAACAAGC 183
Qy 121 TCTCCCGAGAAGGATACAGCTGGAGTCAGTTTAGCGATGTCGAAGAGAACAGGACTGGAAG 180
Db 184 TTTCCCGAGAAGGATACAGCTGGAGTCAGTTTAGTCATGTCGAAGAGAACAGGACTGGAAG 243
Qy 181 CCCCGAGAAGAACTGAACACAGAAAGGAGACCCCGAGTGCATCAATGCGCAACCCATCTCT 240
Db 244 CCCCGAAGGAGCTGAATCGGAGATGGAGACCCCGAGTGCATCAATGCGCAACCCATCTCT 303
Qy 241 GGCACCTGGGGGATAGCCCCGCGGTGAATGGAGACCATGGGCCACAGCAGCAGTTTGGATG 300
Db 304 GGCACCTGGCAGACAGCCCCGCGGTGAATGGAGCACTTGGCGCACAGCAGCAGTTTGGATG 363

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301 CGCGGAGGTAATCCCATGCGAGGTAAGCAAGCGCTGAGAGAGCGCTGGCGATGAGT 360  
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 Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 361 TTGAACGCGGTACCGGAGGCAATTCAGTGATCTAAATCCAGCTTCATATACCCGAG 420  
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 424 TTGAACGCGGTACCGGAGGCAATTCAGTGATCTAAATCCAGCTTCATATACCCGAG 483  
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 544 GGGTGCATATGTCGCTTCTTCTTTTGGGGGGGCACTGTGCGTGGAAAGCGTAGACA 603  
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 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 664 ACCTAGAGCTTTGGATCCAGAGAGCGCGGCTGGGACACTTTTGTGGATCTCTATGGGA 723  
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 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
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 781 CTGACCGTCCACTCACTCTCACTCCACCTTCCACCTTCTGCTGGGCTCACTTTCAGTGGAGTGCAGNACC 840  
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 844 CTGACCGTCCACTCACTCTCACTCCACCTTCCACCTTCTGCTGGGCTCACTTTCAGTGGAGTGCAGNACC 903  
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 904 GCCATTGCCACGAGGAGAAC 924

RESULT 9

US-10-641-643-1430  
 ; Sequence 1430, Application US/10641643  
 ; Publication No. US20040077003A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cocks, Benjamin G.  
 ; Susan G. Stuart  
 ; Jeffrey J. Seilhamer  
 ; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL  
 ; GENE EXPRESSION  
 ; NUMBER OF SEQUENCES: 1508  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESS: INCYTE PHARMACEUTICALS, INC.  
 ; STREET: 3174 PORTER DRIVE  
 ; CITY: PALO ALTO  
 ; STATE: CALIFORNIA  
 ; COUNTRY: USA  
 ; ZIP: 94304  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/10/641,643  
 ; FILING DATE: 14-Aug-2003  
 ; CLASSIFICATION: <Unknown>  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: <Unknown>  
 ; FILING DATE: <Unknown>  
 ; ATTORNEY/AGENT INFORMATION:

NAME: Zeller, Karen J.  
 REGISTRATION NUMBER: 37,071  
 REFERENCE/DOCKET NUMBER: PA-0001 US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (650) 855-0555  
 TELEFAX: (650) 845-4166  
 INFORMATION FOR SEQ ID NO: 1430:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 926 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 IMMEDIATE SOURCE:  
 LIBRARY: GENBANK  
 CLONE: 9510900  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 1430 :  
 US-10-641-643-1430

Query Match 42.4%; Score 737.8; DB 17; Length 926;  
 Best Local Similarity 91.1%; Pred. No. 2e-221;  
 Matches 784; Conservative 0; Mismatches 77; Indels 0; Gaps 0;  
 Qy 1 CACAGAGCAGACCCAGGTGAGTGAGCAGGTGTTTGGACAATGGACTGGTTGAGCCATCT 60  
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
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 61 CTATTATAAANAATGCTCAGAGCAACCGGAGCTGGTGGTGGTCTCTCTCTACAGC 120  
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 124 CTATTATAAANAATGCTCAGAGCAACCGGAGCTGGTGGTGGTCTCTCTCTACAGC 183  
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 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 184 TTTCCGAAAGGATACAGCTGGAGTCACTTACGATGTCGAAAGAGAACAGGACTGAAG 243  
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 244 CCCAGAGAGGACTGAATCGAGATGGAGAGCCCGAGTGGCATCAATGGCAACCCATCT 303  
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 301 CGCGGAGGTAATCCCATGCGAGGTAAGCAAGCGCTGAGAGAGCGCTGGCGATGAGT 360  
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 361 TTGAACGCGGTACCGGAGGCAATTCAGTGATCTAAATCCAGCTTCATATACCCGAG 420  
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 424 TTGAACGCGGTACCGGAGGCAATTCAGTGATCTAAATCCAGCTTCATATACCCGAG 483  
 Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
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 484 GGACAGCATATCAGAGCTTTGAACAGGTAGTGAATGAATCTTTTCGGGATGGGTAAGT 543  
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 481 GGGTGCATATGTCGCTTCTTCTTTTGGGGGGGCACTGTGCGTGGAAAGCGTAGACA 540  
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 544 GGGTGCATATGTCGCTTCTTCTTTTGGGGGGGCACTGTGCGTGGAAAGCGTAGACA 603  
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 721 GCATGACTGTGGCTGTGATCTTCTGCTGGGCTCACTTTCAGTGGAGTGCAGNACA 780  
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 784 GCATGACTGTGGCTGTGATCTTCTGCTGGGCTCACTTTCAGTGGAGTGCAGNACA 843





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; Publication No. US20050064407A1
; GENERAL INFORMATION:
; APPLICANT: Johnson & Johnson Research Pty Ltd
; TITLE OF INVENTION: bcl-2 DNazymes
; FILE REFERENCE: WJF13107942
; CURRENT APPLICATION NUMBER: US/10/479,832A
; CURRENT FILING DATE: 2003-12-08
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 926
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-479-832A-3

Query Match      42.4%; Score 737.8; DB 19; Length 926;
Best Local Similarity 91.1%; Pred. No. 2e-221;
Matches 784; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

Qy 1 CACAGAGCAGACCCAGTGAAGTGAAGTGTGTTGGACAATGGACTGGTTGAGCCCATCT 60
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
64 CAGAGACGAGACTCAGTGAAGTGAAGTGTGTTGGACAATGGACTGGTTGAGCCCATCC 123
Qy 61 CTATTATATAAATGTCTCAGAGCAACCGGAGCTGGTGGTGAATTTCTCTCTACAAAGC 120
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124 CTATTATATAAATGTCTCAGAGCAACCGGAGCTGGTGGTGAATTTCTCTCTCTACAAAGC 183
Qy 121 TCTCCAGCAAGGATACAGCTGGAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAG 180
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
184 TTTCCAGCAAGGATACAGCTGGAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAG 243
Qy 181 CCCAGAGAAACTGAACAGAGAGAGACCCAGTGCATCAATGGCAACCCATCCT 240
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
244 CCCAGAGAGGACTGAATCGGAGTGAAGAGACCCAGTGCATCAATGGCAACCCATCCT 303
Qy 241 GGCACCTGGCGGATAGCCCGCGTGAATGAGACCACTGGCCACAGCAGCTTTGGATG 300
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
304 GGCACCTGGCAGACAGCCCGCGTGAATGAGACCACTGGCCACAGCAGCTTTGGATG 363
Qy 301 CGCGGAGGTAAATCCCATGGCAGAGTGAAGCAAGCCCTGAGAGAGCTGGCGATGAGT 360
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
364 CGCGGAGGTGATCCCATGGCAGAGTGAAGCAAGCCCTGAGGAGGAGCAGGCGCAGT 423
Qy 361 TTGAACCTCGGTACCGGAGAGCATTCAGTGTATCAATCCAGCTTCATATAACCCAG 420
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
424 TTGAACCTCGGTACCGGAGAGCATTCAGTGTATCAATCCAGCTTCATATAACCCAG 483
Qy 421 GGACAGCATATCAGAGCTTTGAACAGGTAGTGAATGAATCTCTTTGGGATGGGTAAACT 480
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
484 GGACAGCATATCAGAGCTTTGAACAGGTAGTGAATGAATCTCTTTGGGATGGGTAAACT 543
Qy 481 GGGGTGCGCATTTGTGGCTTCTCTCTTTGGGGGGGCACTGTGCGTGAAGAGCGTAGACA 540
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
544 GGGGTGCGCATTTGTGGCTTCTCTCTTTGGGGGGGCACTGTGCGTGAAGAGCGTAGACA 603
Qy 541 AGGAGATGAGGTATTTGTGTAGTGGATTCGAAGTTGGATGGCCACCTTACCTGAATGACC 600
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
604 AGGAGATGAGGTATTTGTGTAGTGGATTCGAAGTTGGATGGCCACCTTACCTGAATGACC 663
Qy 601 ACCTAGAGCTTTGGATCCAGGAGAAACCGCGCTGGGACACTTTTGTGGATCTCTACGGGA 660
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
664 ACCTAGAGCTTTGGATCCAGGAGAAACCGCGCTGGGATACCTTTTGTGGATCTCTATGGGA 723
Qy 661 ACAATGACAGCAGCGAGAGCCGGAAGCCAGGAGCGTTTCAACCGCTGGTTCCTGACGG 720
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
724 ACAATGACAGCAGCGAGAGCCGGAAGCCAGGAGCGTTTCAACCGCTGGTTCCTGACGG 783
Qy 721 GCATGACTGTGGCTGTGTGTCTGTCTGGGCTCACTCTCAGTCCGAAGTGACACAGACA 780
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
784 GCATGACTGTGGCTGTGTGTCTGTCTGGGCTCACTCTCAGTCCGAAGTGACACAGACA 843
Qy 781 CTGACCGTCCACTCACTCTCACTCCCACTTGGCCCCCACCACAACCTCTCTCTTCAGCC 840
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Db 844 CTGACCATCCACTCTACCCCTCCACCCCTCTCTCTGTCTCCACCACATCTCTCCGTCCAGCC 903
Qy 841 ACCATTGCTACCCAGGAGAAC 861
Db 904 GCCATTGCCACCCAGGAGAAC 924

RESULT 14
US-10-388-360-351
; Sequence 351, Application US/10388360
; Publication No. US2003022528A1
; GENERAL INFORMATION:
; APPLICANT: GENOMIC HEALTH
; APPLICANT: Baker, Joffre B.
; APPLICANT: Cronin, Maureen T.
; APPLICANT: Kiefer, Michael C.
; APPLICANT: Shak, Steve
; APPLICANT: Walker, Michael Graham
; TITLE OF INVENTION: GENE EXPRESSION PROFILING IN BIOPSIED TUMOR TISSUES
; CURRENT APPLICATION NUMBER: US/10/388,360
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 60/412,049
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: US 60/364,890
; PRIOR FILING DATE: 2002-03-13
; NUMBER OF SEQ ID NOS: 384
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 351
; LENGTH: 2386
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-388-360-351

Query Match      38.0%; Score 661.4; DB 17; Length 2386;
Best Local Similarity 69.5%; Pred. No. 3.4e-197;
Matches 1222; Conservative 0; Mismatches 291; Indels 246; Gaps 14;

Qy 1 CACAGACAGACCCAGTGAAGTGAAGTGTGTTGGACAATGGACTGGTTGAGCCCATCT 60
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Db 356 CTATTATATAAATGTCTCAGAGCAACCGGAGCTGGTGGTGAATTTCTCTCTACAAAGC 415
Qy 121 TCTCCAGAAAGGATACAGCTGGAGTCACTTTAGCGATGTCGAAGAGAACAGGACTGAAG 180
Db 416 TTTCCAGAAAGGATACAGCTGGAGTCACTTTAGTAGTGTGGAAGAGAACAGGACTGAAG 475
Qy 181 CCCAGAGAAACTGACACAGAGAGAGACCCCGAGTGCATCAATGGCAACCCATCCT 240
Db 476 CCCAGAGAGGACTGAATCGGAGATGAGAGACCCCGAGTGCATCAATGGCAACCCATCCT 535
Qy 241 GGCACCTGGCGGATGAGCCCGGTGAATGAGACCACTGGCCACAGCAGCAGTGTGGATG 300
Db 536 GGCACCTGGCAGACAGCCCGCGGTGAATGGAGCCACTGGCCACAGCAGCAGTGTGGATG 595
Qy 301 CGCGGAGGTAAATCCCATGGCAGCAGTGAAGCAAGCGCTGAGAGAGCGCTGGCGATGAGT 360
Db 596 CGCGGAGGTGATCCCATGGCAGCAGTGAAGCAAGCGCTGAGGAGAGCGCAGGCGCAGT 655
Qy 361 TTGAACCTGGGTACCGGAGAGCATTCAGTGTCTAAATCCAGCTTCATATACCCAG 420
Db 656 TTGAACCTGGGTACCGGAGAGCATTCAGTGTCTAAATCCAGCTTCATATACCCAG 715
Qy 421 GGACAGCATATCAGAGCTTTGAACAGGTAGTGAATGAATCTCTTTGGGATGGGTAAACT 480
Db 716 GGACAGCATATCAGAGCTTTGAACAGGTAGTGAATGAATCTCTTTGGGATGGGTAAACT 740
Qy 481 GGGGTGCGCATTTGTGGCTTCTCTCTTTGGGGGGGCACTGTGCGTGAAGAGCGTAGACA 540
Db 741 ----- 740

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Db 741 ----- 740  
QY 601 ACCTAGAGCCTTTGGATCCAGGAGAACGCGCTGGGACACTTTTGTGGATCTCTACGGGA 660  
Db 741 -----GGATACATTTTGTGGAATCTCTATGGGA 766  
QY 661 ACAATGACAGACCGAGAGCCGGAAGAGCGGTTTCAACCGCTGGTTCTCTGACGG 720  
Db 767 ACAATGACAGACCGAGAGCCGGAAGAGCGGTTTCAACCGCTGGTTCTCTGACGG 826  
QY 721 GCATGACTGTGGCTGGTGTAGTTCTGTCTGGGCTCACTCTTCACTGCGGAAGTACCAAGACA 780  
Db 827 GCATGACTGTGGCTGGGCTGGTGTCTGTCTGGGCTCACTCTTCACTGCGGAAGTACCAAGACA 886  
QY 781 CTGACCGTCCACTCACTCTCACTCCACCTTGCCTCCACCACTCACTCTCTCTTCAGCC 840  
Db 887 CTGACCATCCACTCACTCTCCACCTTGCCTCCACCACTCACTCTCTCTTCAGCC 946  
QY 841 ACCAATTGCTACAGGAGAACCACTACATGCAACTCAACGCGCTTCCCTATTATAGGGTT 900  
Db 947 GCCATTGCCACAGGAGAACCACTACATGCAAGCCATGCCACCTGCCCATCAACAGGGTT 1006  
QY 901 GGGCTTAGACGGAGTCCCTCGAGTTAGCTTTCTAGAACTCAACAGCTTCTGTGAAAGC 960  
Db 1007 GGGCTTAGAGTGGTCCCTCGAGTTAGCTTTCTAGAACTTATCACTCTCTGTGAGA-- 1064  
QY 961 CACCTTCCCTCCACATCTCACTTCCCTGGGCTCAAACTCAAGGTTTTCCTTCAGAT 1020  
Db 1065 -----CCCCACACCTCAGTTCCCTTGGCTCAGAAATTCACAA-AAATTCACAAAT 1116  
QY 1021 CAGCTCTTTGGAGGTGCGAGAGTGGGAAGGGGTGTCTAGAGGG--AGAAGAGCCTGC 1078  
Db 1117 CTGTCCAAAGAGGCTGCGAGGTATGGAAGGGTTGTGGCTGGGGCAGAGGGCCCTAC 1176  
QY 1079 CTTGTTGTGGAGCCCTGAATTAACCTCTGAGCCTCTCGGGAATGCTTTTCTGGCAGGGAGC 1138  
Db 1177 CTGATTGTGCAACCCCT--TACCCCTTAGCCTCCCTGAAATGTTTTTCTGCCAGGGAGC 1234  
QY 1139 TGGAGAGCTCTAAACCTCTTCCCT---CAGAGACTAGATGCTGTTGTTTGTGATGTG 1194  
Db 1235 TTGAAGTTTTCAGAACTCTTCCCTCCAGAAAGGAGACTAGATGCTGTTTGTGATGT 1294  
QY 1195 TGTGGCTCAGAAATGATTCATTTCCCTCTGCTGTCTGCTGGGGGGCTCTCTCTTC 1254  
Db 1295 TGTGGCTCAGAAATGATTCATTTCCCTCCCTCTCTCCCACTAACTGAGGTTCCCTTT 1354  
QY 1255 CCATCTCCACCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCT 1314  
Db 1355 CC--TTCCATCCCTACCCCTTAAGAGCCATTTAGGGGCCACTTT-----TG 1398  
QY 1315 ACTAAATATGAGGCTGCTGGGATACAGGCAAGGACC-----TCTCCCTCCCTGCT 1368  
Db 1399 ACTAGGATTCAGGCTGCTGGGATTAAGATGCAAGGACCAAGGACTCCCTCTCTCACTCT 1458  
QY 1369 GGCCTGGGCA--AGCCCTCACTCTGCTGCTGATGTTCTCTGAGGCTCTGGCTAGAGTC 1427  
Db 1459 GGAATGGGTAGATCTCACTCTCCCTAGTCCAAATGCTCTCCAGAGGCTCTGGCTAGAGC 1518  
QY 1428 CAGCCCAACCAAGGAG--GAGGAGCGGAGCTGGGAAAGTCCACCTTCGAGAGGCTGA 1484  
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QY 1485 GCGGCTCTTGGGCTTAGACACACCCAGATGCTTCTCCACCCCTCCCTCCCTCCCTCCATGG 1544  
Db 1579 GTGGGCTTTGAGTTTCAAGCACCCTAGTCCCTTCCCTCCCTCCCTCCCTCCCTCCCT--CC 1629  
QY 1545 TGACATGACTGAGGAGCAACTGGGCCACGCTAGGTGGCCAGAGCTGTTAATGACTT 1604  
Db 1630 ATGACCATACTGAGGAGCAACTGGGCCCAAGACAGATGCCCCCAGAGCTGTTTATGGCT 1689

QY 1605 CAGCTGCTCACTTCTCTGCAAGATCAGCCTGTGCACTTTTGGCTTGGTCTGGCCACA 1664  
Db 1690 CAGCTGCTCACTTCTCTACAGAGCAGCCTGTGCACTTTTGGCTTGG--CTGCTCCT 1746  
QY 1665 GGGTCCAGGAGTCTGCGCTTAGCCAGAACTGAGAGGAAGCTTACA-GCGCAGCTATGG 1723  
Db 1747 CATGCTGGTTTCAGGGGACTCAGCCCTGAGGTGAAGGGAGCTATCAGGAACAGCTATGG 1806  
QY 1724 GAGCCTTGGGGCTTCCCT 1742  
Db 1807 GAGCCCCAGGGCTTCCCT 1825  
RESULT 15  
US-10-388-934-539  
; Sequence 539, Application US/10388934  
; Publication No. US20040005547A1  
; GENERAL INFORMATION:  
; APPLICANT: Boess, Franziska  
; APPLICANT: Suter-Dick, Laura  
; APPLICANT: Wolf, Detlef  
; TITLE OF INVENTION: BIOMARKERS AND EXPRESSION PROFILES FOR TOXICOLOGY  
; FILE REFERENCE: 21199  
; CURRENT APPLICATION NUMBER: US/10/388,934  
; CURRENT FILING DATE: 2003-03-14  
; PRIOR APPLICATION NUMBER: 02005336.9  
; PRIOR FILING DATE: 2002-03-14  
; PRIOR APPLICATION NUMBER: 02015657.6  
; PRIOR FILING DATE: 2002-07-17  
; NUMBER OF SEQ ID NOS: 862  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 539  
; LENGTH: 1748  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus (No. US20040005547A1way rat)  
US-10-388-934-539

Query Match 36.5%; Score 636; DB 17; Length 1748;  
Best Local Similarity 100.0%; Pred. No. 3.1e-189;  
Matches 636; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CACAGACGACCCAGTGTGACAGGTGTTTGGCAATGGACTGGTTCAGGCCATCT 60  
Db 93 CACAGACGACCCAGTGTGACAGGTGTTTGGCAATGGACTGGTTCAGGCCATCT 152  
QY 61 CTATTATAAATCTCTCAGAGCAACCGGAGCTGGTGTGACTTTCTCTCTACAAGC 120  
Db 153 CTATTATAAATCTCTCAGAGCAACCGGAGCTGGTGTGACTTTCTCTCTACAAGC 212  
QY 121 TCTCCAGAAAGGATACAGCTGGAGTCAAGTGTTCGAGATGTGGAAGAGAACAGGACTGAAG 180  
Db 213 TCTCCAGAAAGGATACAGCTGGAGTCAAGTGTTCGAGATGTGGAAGAGAACAGGACTGAAG 272  
QY 181 CCCAGAGAACTCAACCAAGAGGAGAGCCCGAGTGCCTCAATGGCAACCCATCCT 240  
Db 273 CCCAGAGAACTCAACCAAGAGGAGAGCCCGAGTGCCTCAATGGCAACCCATCCT 332  
QY 241 GGCACCTGGCGATAGCCCGGCTGAATGAGGACCTTGGCCACAGCAGAGTGTGGATG 300  
Db 333 GGCACCTGGCGATAGCCCGGCTGAATGAGGACCTTGGCCACAGCAGAGTGTGGATG 392  
QY 301 CGCGGAGGTAATCCCATGACAGTGAAGCAAGCGCTGAGAGAGGCTGGCGATGAGT 360  
Db 393 CGCGGAGGTAATCCCATGACAGTGAAGCAAGCGCTGAGAGAGGCTGGCGATGAGT 452  
QY 361 TTGAATCGCGTACCGGAGAGCATTCAGTGTATTAACATCCAGCTTCATATACCCAG 420  
Db 453 TTGAATCGCGTACCGGAGAGCATTCAGTGTATTAACATCCAGCTTCATATACCCAG 512  
QY 421 GGACAGCATATCAGAGCTTTGAACAGGTAGTGAATGAATCTTTTCGGGATGSGGTAACT 480  
Db 513 GGACAGCATATCAGAGCTTTGAACAGGTAGTGAATGAATCTTTTCGGGATGSGGTAACT 572

Qy	481	GGGTCGCATTGTGGCCCTTCTTCTCCTTTGGCGGGCACTGTGGCTGGAAGCGTAGACA	540
Db	573	GGGTCGCATTGTGGCCCTTCTTCTCCTTTGGCGGGCACTGTGGCTGGAAGCGTAGACA	632
Qy	541	AGGAGATGCAGGTATTGTGAGTCGGATTGCAAGTTGGATGGCCACCTACCTGAATGACC	600
Db	633	AGGAGATGCAGGTATTGTGAGTCGGATTGCAAGTTGGATGGCCACCTACCTGAATGACC	692
Qy	601	ACCTAGAGCCTTGGATCCAGGAGAACGGCGGCTGGG	636
Db	693	ACCTAGAGCCTTGGATCCAGGAGAACGGCGGCTGGG	728

Search completed: March 31, 2005, 06:13:03  
Job time : 6364 secs

Result No.	Query			DB	ID	Description
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	2	742.6	42.6	767	7	CK483979 AGENCOURT
	3	727.4	41.8	1087	5	BU156982 AGENCOURT
	4	727	41.7	919	5	BQ948029 AGENCOURT
	5	726.4	41.7	878	5	BQ888053 AGENCOURT
	6	722.4	41.5	997	5	BQ052167 AGENCOURT
	7	716.2	41.1	989	5	BX441570 AGENCOURT
	8	714.8	41.0	1002	4	BM549716 AGENCOURT
	9	707.2	40.6	758	7	CO396360 AGENCOURT
	10	707	40.6	1134	7	CK359456 BX359456
	11	704.4	40.4	798	7	CK000319 AGENCOURT
	12	696.2	40.0	922	5	BQ924197 AGENCOURT
	13	693.6	39.8	732	5	BQ053776 UI-M-PD0-
	14	693.4	39.8	1035	4	BU1409987
	15	691.8	39.7	826	7	CK482364 AGENCOURT
C	16	690	39.6	1045	4	BM811650 AGENCOURT
	17	686.2	39.4	724	7	CF730725 UI-M-GZ0-
	18	685.2	39.3	735	5	BQ053967 UI-M-PD0-
	19	682.2	39.2	720	5	BU709510 UI-M-EV0-
	20	680.8	39.1	798	7	CK481691 AGENCOURT
	21	680.2	39.0	719	5	BQ443341 UI-M-EV0-
	22	676.4	38.8	721	5	BU703310 UI-M-PD0-
	23	668.4	38.4	913	4	BG344406 602356535
	24	663.2	38.1	700	6	CA751645 UI-M-PD0-

Qy 85 ACCGGAGCTGGTGGTTGACT

3

7



Db 1 ACCGGAGCTGGTGGTCTGACTTTCTCTCTCAAGCTTTCCAGAAAGATACAGCTGGA 60  
Qy 145 GTCAGTTTAGCGATGTCGAGAGACAGGACTGAAGCCCGCAGAGAACTGAACAGAAA 204  
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Db 121 GGGAGACCCCGAGTCCCATCAATGCAACCCACTCTGCGACCTGCGGATAGCCCGCGG 180  
Qy 265 TGAATGGAGCCACTGCGCCACAGCAGCAGTTTGGATGCGCGGAGGTAATCCCATGGCAG 324  
Db 181 TGAATGGAGCCACTGCGCCACAGCAGCAGTTTGGATGCGCGGAGGTAATCCCATGGCAG 240  
Qy 325 CAGTGAACCAAGCGCTGAGAGAGGCTGGCGATGAGTTTGAATCGCGGTACCGGAGAGAT 384  
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Qy 385 TCAGTGATCTTAACATCCAGCTTTATATAACCCAGGAGACAGCATATCAGAGCTTTGAAC 444  
Db 301 TCAGTGATCTTAACATCCAGCTTTATATAACCCAGGAGACCGGTATCAGAGCTTTGAGC 360  
Qy 445 AGGTAGTGAATGAACCTTTTGGGATGGGTAAACTGGGGTGGCATTTGGCCCTTTCT 504  
Db 361 AGGTAGTGAATGAACCTTTTGGGATGGGTAAACTGGGGTGGCATTTGGCCCTTTCT 420  
Qy 505 CTTTGGCGGGGACCTGTGCTGGAAGCGGTAGACAAGAGATGAGGTATTTGGAGTC 564  
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Qy 625 ACGCGGCTGGGACACTTTTGTGGATCTCTACGGGAACAATGCAGCAGCCGAGAGCCGGA 684  
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Qy 685 AAGGCCAGAGGTTTCAACCGCTGGTCTGACCGGGATGACGTGCTGCTGGTGTAGTTC 744  
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Qy 745 TGCTGGGCTCACTCTTTCAGTGGAGTGCACAGACACTGACGCTCACTACCTCTCACC 804  
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Qy 805 TCCCACTTGGCCCCCACCACCACTCTCTTTCAGCACCATTGCTTACCGAGAGAACCACT 864  
Db 721 TCCCACTTGGCCCCCACCACCACTCTCTTTCAGCACCATTGCTTACCGAGAGAACCACT 780  
Qy 865 ACATGCAACTCAGC-CGCCCTTATATAGGTTGGG--CCTAGACGGAGTCCCC 919  
Db 781 ACATGCAACTCAGC-CGCCCTTATATAGGTTGGG--CCTAGACGGAGTCCCC 838

RESULT 2  
LOCUS CK483979 767 bp mRNA linear EST 14-JAN-2004  
DEFINITION AGENCOURT 17635534 NIH MGC 235 Rattus norvegicus cDNA clone  
IMAGE:7110877 5', mRNA sequence.  
ACCESSION CK483979  
VERSION CK483979.1 GI:40828327  
KEYWORDS EST.  
SOURCE Rattus norvegicus (Norway rat)  
ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.  
REFERENCE 1 (bases 1 to 767)  
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)

COMMENT

Contact: Daniela S. Gerhard, Ph.D.  
Office of Cancer Genomics  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: cgabs-remail.nih.gov  
Tissue Procurement: Howard Jacobs  
cDNA Library Preparation: Express Genomics  
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLAM14978 row: 1 column: 11  
High quality sequence stop: 675.  
Location/Qualifiers  
1. .767  
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/db\_xref="taxon:10116"  
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/tissue\_type="kidney, pooled"  
/lab\_host="DH10B TorA"  
/clone\_lib="NIH\_MGC\_235"  
/note="Organ: kidney; Vector: pExpress-1; Site 1: EcoRV;  
Site 2: NotI; RNA obtained from pooled kidney tissue from  
a mix of male and female animals at 8 wk old. Tissues were  
snap-frozen before RNA extraction and purification  
(TRI-reagent method). cDNA was primed using oligo-dT  
primer: 5'-pGACTAGTCTAGTCGAGCGCGCC(T)25-3' and  
cloned into the EcoRV/NotI sites of pExpress-1.  
Size-selection >1.4kb resulted in an average insert size  
of 2.2 kb. This primary library is non-normalized  
(normalized primary library is NIH\_MGC\_236) and was  
constructed by Express Genomics (Frederick, MD). Note:  
this is a NIH\_MGC library."

FEATURES

source

ORIGIN

Query Match 42.6%; Score 742.6; DB 7; Length 767;  
Best Local Similarity 99.2%; Pred. No. 3.9e-192;  
Matches 757; Conservative 0; Mismatches 2; Gaps 1;

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Qy 414 ACCCCAGGAGCAGCATATCAGAGCTTTTGAACAGGTAGTGAATGAATCTTTTCGGGATGGG 473  
Db 181 ACCCCAGGAGCAGCATATCAGAGCTTTTGAACAGGTAGTGAATGAATCTTTTCGGGATGGG 240  
Qy 474 GTAAACTGGGGTGCATTTGGCCCTTCTTCTTTTGGCGGGGCACTGTGCTGGGAAAGC 533  
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Qy 594 AATGACCACTTAGAGCTTTGGATCCAGGAGAACCGCGCTGGGACACTTTTGTGGATCTC 653  
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Qy 834 TTACGCCACCAATTCTTACCAAGGAGAACCACTACATGCAACTCAGCCCTTCCCTATTTA 893
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Qy 954 TGAAGGCACCTTCCCGCCACATCTCAGTTCCCTTGGCCTCAA 996
Db 721 TGAAGGCACCTTCCCGCC--CATCTCAGTTCCCTTGGCTCAAA 761

RESULT 3
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LOCUS AGENCOURT 7186902 NIH_MGC_100 Homo sapiens cDNA clone IMAGE:6001882
5', mRNA sequence.
ACCESSION BUI56982
VERSION BUI56982.1 GI:22670514
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1087)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: CGAP (Stanford)
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LCM2269 row: d column: 11
High quality sequence stop: 721.
Location/Qualifiers
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/organism="Homo sapiens"
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/notes="Organ: liver; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Size-selected >500bp for average insert size
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."

FEATURES
source
Query Match 41.8%; Score 727.4; DB 5; Length 1087;
Best Local Similarity 82.2%; Pred. No. 6.3e-188;
Matches 901; Conservative 0; Mismatches 174; Indels 21; Gaps 5;
Qy 140 CTGGAGTCAGTTAGCGATGTGGAAGAGAACGAGACTGAGCCCCCAGAGAACTGAACC 199

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Db 1 CTGGAGTCAGTTAGTGATGTGGAAGAGAACGAGACTGAGGCCCCAGAGGGACTGAATC 60
Qy 200 AGAAAGGGAGACCCCCAGTGCCTCAATGCAACCCATCTTGGCACTCTGGCGATAGCCCC 259
Db 61 GGAGATGGAGACCCCCAGTGCCTCAATGCAACCCATCTTGGCACTCTGGCAGACAGCCC 120
Qy 260 CGCGGTGAATGGAGCCACTTGGCCACAGCAGAGTTTGGATGCGCGGGAGGTAAATCCCAT 319
Db 121 CGCGGTGAATGGAGCCACTTGGCCACAGCAGAGTTTGGATGCGCGGGAGGTAAATCCCAT 180
Qy 320 GGCAGCAGTCAAGCAAGCGCTGAGAGAGGTGGCGATGAGTTTGAATCGCGGTACCGGAG 379
Db 181 GGCAGCAGTAAAGCAAGCGCTGAGGGAGGCGAGGCGAGGTTTGAATCGCGGTACCGGCG 240
Qy 380 AGCAATTCAGTGATCTTAACATCCAGCTTCAATAACCCAGGGACAGCATATCAGAGCTT 439
Db 241 GGCATTCAGTGACTGACATCCAGCTCCACATCACCCAGGGACAGCATATCAGAGCTT 300
Qy 440 TGAACAGGTAGTGAATGAATCTTTTCGGGATGGGGTAAACTTGGGGTGCATTTGGCGCTT 499
Db 301 TGAACAGGTAGTGAATGAATCTTTTCGGGATGGGGTAAACTTGGGGTGCATTTGGCGCTT 360
Qy 500 CTTCTCCTTTGGCGGGCACTGTGCGTGAAGAGGTAGACAGAGAGTTCAGGTATTGGT 559
Db 361 TTTCTCCTTTGGCGGGCACTGTGCGTGAAGAGGTAGACAGAGTTCAGGTATTGGT 420
Qy 560 GAGTCGGATTCGAAGTTGGATGGCCACTCTCTGAATGACCACTAGAGCTTCGATCCA 619
Db 421 GAGTCGGATTCGAAGTTGGATGGCCACTCTCTGAATGACCACTAGAGCTTCGATCCA 480
Qy 620 GGAGAACGGGGCTGGGACACTTTTGTGGATCTCTACGGGAACTTACAGAGCCGAGAG 679
Db 481 GGAGAACGGGGCTGGGATACTTTTGTGGAACTCTATGGGAACTTATGGCAGCGAGAG 540
Qy 680 CCGAAGAGGCGCAGAGCGTTTCAACCGCTGTCTCTGACGGGCACTGCTGGCTGGTGT 739
Db 541 CCGAAGAGGCGCAGGAAAGCTTCAACCGCTGTCTCTGACGGGCACTGCTGGCGGGCT 600
Qy 740 AGTTCTCTGGGCTCACTCTTCACTCGGAGTACACAGACTCACTCCCTCACTCACTC 799
Db 601 GGTTCCTCTGGGCTCACTCTTCACTCGGAGTACACAGACTCACTCCCTCACTCACTC 660
Qy 800 TCACCTCCCACTTGGCCCCCAACCACTCTCTCTCAGCCCACTTGTCTACAGGAGAA 859
Db 661 TCCCAACCCCTTCTCTGCTCCACACATCTCTCCGTCAGCGCCCATTTGCCACAGGAGAA 720
Qy 860 CCATCATGCAACTCAAGCCCTTCCCTTATATATAGGTTGGGCTTAGACGGAGTCCCC 919
Db 721 CCATCATGCAAGCCCATGCCCACCTGCCCACATCAAGGGTTGGGCCCAAGATCTGCTCCCT 780
Qy 920 TGCAGTTAGCTTTCTAGAACTTACACGCTTCTCTGGAAGCCACTTCCCTCCCACTC 979
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Qy 980 AGTTCCCTTGGGCTCAAACTCAAGGTTTCTCTCAGATCAGCTCTCTGGAGGCTGGC 1039
Db 832 AGTTCCCTTGGGCTCAGAAATTCAGAA-----ATTTTCAGAAATCTGTCCAAGGAGCTGGC 888
Qy 1040 AGGAGTGGGAAGGG---GTGTGCTAGAGGGAGAGAGCTCTCTTGTGTGGGACCTGT 1096
Db 889 AGGTATGGGAAGGGTTGTGTGCTGGGCGCAGAGGGCCCTACCTGATTTGGNGGCACTT 948
Qy 1097 ATTACCCCTGAGCTCTCGGGAAATGCTTTTCTGGAGGGAGCTGAGAGCTCTCTTAACC 1156
Db 949 TACCCCTTAGCTCCCTGGAAATGCTTTTCTGCGAGGGAGCTTGAAGATTTTCAGAAAC 1008
Qy 1157 TCTTCCCCCA--GAGACTAGATTGCC-----TTGGTTTGTGTTGTGCTCAGAAATG 1210
Db 1009 TCTTCCCCGAAAGGAGACTAGATGGGCTTGGTGGTTTGAAGGTTGGGGCTCCANAAATG 1069
Qy 1211 ATCCATTTCCCATTTCT 1226

```









TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Daniela S. Gerhard, Ph.D.  
Office of Cancer Genomics  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Drs. Josef Lazar & Howard Jacob, Medical  
College of Wisconsin  
cDNA Library Preparation: Express Genomics  
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: L14W15368 row: o column: 02  
High quality sequence start: 17  
High quality sequence stop: 544.  
Location/Qualifiers  
1. 758  
/organism="Rattus norvegicus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10116"  
/clone="IMAGE:7315132"  
/sex="both"  
/tissue type="Brain - Pooled from several tissues from one  
or more individuals"  
/lab host="DH10B Tona"  
/clone\_lib="NIH\_MGC\_254"  
/note="Organ: brain/CNS; Vector: pExpress-1; Site: 1:  
EcorV; Site 2: NotI; RNA obtained from brain tissue of 8  
wk old animal. Tissues were snap-frozen and kept at -80C  
before RNA extraction and purification (Tri-reagent  
method). cDNA was primed using oligo-dT primer:  
5'-PGACTAGTTCAGTTCGAGCGGCCCTT)25-3' and cloned into  
the EcorV/NotI sites of pExpress-1. Size-selection >1.25kb  
resulted in an average insert size of 2.18 kb. This  
primary library is not normalized (normalized library is  
NIH\_MGC\_255) and was constructed by Express Genomics  
(Frederick, MD). Note: this is a NIH\_MGC library"

ORIGIN  
Query Match 40.6%; Score 707.2; DB 7; Length 758;  
Best Local Similarity 99.2%; Pred. No. 2e-182;  
Matches 720; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

Qy 534 CTGACCAAGGAGATGACGATTTGGTGTGAGTCGGATTGCAAGTTGGATGGCCACCTTACCTG 593  
Db 34 GGATCCAAAGGAGATGACGATTTGGTGTGAGTCGGATTGCAAGTTGGATGGCCACCTTACCTG 93  
Qy 594 AATGACCACTTAGACCTTGGATCAGGAGAACGGCGCTGGGACACCTTTTGTGATCTC 653  
Db 94 AATGACCACTTAGACCTTGGATCAGGAGAACGGCGCTGGGACACCTTTTGTGATCTC 153  
Qy 654 TACGGGAACATGACGAGCGGAGCGGAAAGCCAGGACGCTTCAACCGCTGGTTC 713  
Db 154 TACGGGAACATGACGAGCGGAGCGGAAAGCCAGGACGCTTCAACCGCTGGTTC 213  
Qy 714 CTGACGGGCATGACTGTGGCTAGTTCGTGTGGCTCAGCTCTTTCAGTCGGAAGTGA 773  
Db 214 CTGACGGGCATGACTGTGGCTAGTTCGTGTGGCTCAGCTCTTTCAGTCGGAAGTGA 273  
Qy 774 CCAGACACTGACCTGCTCAGCTCTCAGCTCCACCTTGGCCGCCACCACTCTCTC 833  
Db 274 CCAGACACTGACCTGCTCAGCTCTCAGCTCCACCTTGGCCGCCACCACTCTCTC 333  
Qy 834 TTACGACCACTTGTCTACAGGAGAACCACTACATGCAACTCAGCCCTTCCCTATT 893  
Db 334 TTACGACCACTTGTCTACAGGAGAACCACTACATGCAACTCAGCCCTTCCCTATT 393  
Qy 894 TAGGTTGGGCTTAGACGAGGTCCTCTGAGTTAGTCTTCTAGATCTTACACGCTCTG 953  
Db 394 TAGGTTGGGCTTAGACGAGGTCCTCTGAGTTAGTCTTCTAGATCTTACACGCTCTG 453

Qy 954 TGAAGCCACCTTCCCCCACCACATCTCAGTTTCCCTTGGCTCAAACTCACAAGGTTTTTC 1013  
Db 454 TGAAGCCACCTTCCCCCACCACATCTCAGTTTCCCTTGGCTCAAACTCACAAGGTTTTTC 513  
Qy 1014 CTCAGATCAGCTCCTTGGAGGCTGGCAGGAGTGGGAAGGGGTGTGCTAGAGGGAGAAGAG 1073  
Db 514 CTCAGATCAGCTCCTTGGAGGCTGGCAGGAGTGGGAAGGGGTGTGCTAGAGGGAGAAGAG 573  
Qy 1074 CTTGCCCTTGTGTGGGACCCCTGATTACCCCTGAGCCCTCTCGGGAATGCTTTTCTGGCAG 1133  
Db 574 CTTGCCCTTGTGTGGGACCCCTGATTACCCCTGAGCCCTCTCGGGAATGCTTTTCTGGCAG 633  
Qy 1134 GGAGCTGGAGAGCTCTCTAAACCTTTCGCCCCAGAGACTAGATTGCTTGGTGTGATGT 1193  
Db 634 GGAGCTGGAGAGCTCTCTAAACCTTTCGCCCCAGAGACTAGATTGCTTGGTGTGATGT 693  
Qy 1194 GTGTGGCTCAGAAATTGATCCATTTCCTGCTGTGTCCTCGGGCGGCTCTCTCCTT 1253  
Db 694 GTGTGGCTCAGAAATTGATCCATTTCCTGCTGTGTCCTCGGGCGGCTCTCTCCTT 752  
Qy 1254 CCGATC 1259  
Db 753 CCGATC 758

RESULT 10  
BX359456 1134 bp mRNA linear EST 08-APR-2004  
LOCUS BX359456 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA  
DEFINITION Clone CSOD1057YN09 5-PRIME, mRNA sequence.  
ACCESSION BX359456  
VERSION BX359456.2 GI:46287636  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1134)  
AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished (2001)  
COMMENT On May 5, 2003 this sequence version replaced gi:30368313.  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by Life Technologies, a  
division of Invitrogen. This sequence belongs to sequence cluster  
9697.r  
For more information about this cluster, see  
http://www.genoscope.cns.fr/cdna?n=CSOD1057CG05QPlkc=9697.r.

FEATURES  
Location/Qualifiers  
1. 1134  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="CSOD1057YN09"  
/tissue type="PLACENTA COT 25-NORMALIZED"  
/clone\_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"  
/note="1st strand cDNA was primed with a NotI-oligo(dT)  
primer. Five prime end enriched, double-strand cDNA was  
digested with Not I and cloned into the Not I and EcoR V  
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN  
Query Match 40.6%; Score 707; DB 5; Length 1134;  
Best Local Similarity 91.5%; Pred. No. 2.5e-182;  
Matches 760; Conservative 0; Mismatches 70; Indels 1; Gaps 1;



1	QY	CACAGACAGACCCAGTGCAGTGAGCAGGTTGTTTGGACAATGACATGGTTGAGCCCATCT	60
213	DB		
213	DB	CAGACAGACAGACTCAGTGCAGTGAGCAGGTTGTTTGGACAATGACATGGTTGAGCCCATCC	272
61	QY	CTATTATAAAAATGTCTCAGAGCAACCGGGAGCTGGTGGTTGACTTTCTCTCTCAACAG	120
273	DB	CTATTATAAAAATGTCTCAGAGCAACCGGGAGCTGGTGGTTGACTTTCTCTCTCAACAG	332
121	QY	TTCTCCAGAAAGGATACAGCTGGAGTCACTTTAGCGATGTGGAAGAGAACAGGACTGAA	180
333	DB	TTTCCAGAAAGGATACAGCTGGAGTCACTTTAGTGTATGTGGAGAGAAACAGGACTGAG	392
181	QY	CCCCAGAGAAACTCAACACAGAAAGGAGACCCCGACGTGCATCAATGGCAACCCATCTCT	240
393	DB	CCCCAGAGGAGACTGATTCGAGATGAGAGACCCCGACGTGCATCAATGGCAACCCATCTCT	452
241	QY	GGCACCCTGGCGGATAGCCCGCGGTGAATGGAGCCACTGGCCACAGCAGCAGTTTGGATG	300
453	DB	GGCACCCTGGCAGACAGCCCGCGGTGAATGGAGCCACTGGCCACAGCAGCAGTTTGGATG	512
301	QY	CCGGGGAGGTAATCCCATGGCAGCAGTGAAGCAAGCGCTTGAGAGAGGCTGGCGATGAGT	360
513	DB	CCCGGGAGGTGATCCCCATGGCAGCAGTGAAGCAAGCGCTTGAGAGAGGCGAGCGAT	572
361	QY	TTTGAACCTGGGTACCGGAGAGCATTCAGTGTATTAACATCCAGCTTTCATATAACCCACG	420
573	DB	TTTGAACCTGGGTACCGCGGGCATTTCACTGACCTGACATCCAGCTCCACATCACCCACG	632
421	QY	GGACAGCATATCAGAGCTTTGAACAGGTAGTGAATGAACTCTTTTCGGGATGGGGTAAACT	480
633	DB	GGACAGCATATCAGAGCTTTGAACAGGTAGTGAATGAACTCTTTTCGGGATGGGGTAAACT	692
481	QY	GGGGTGCATTTGTGGCCTTCTTCTCTTTTGGCGGGGCACTGTGGGTGGAAAGCGTGAGCA	540
693	DB	GGGGTGCATTTGTGGCCTTCTTCTCTTTTGGCGGGGCACTGTGGGTGGAAAGCGTGAGCA	752
541	QY	AGGAGATGCAGGTATTGGTGTAGTGGATTGCAAGTTGGATGGCCACCCTACTCTGAATGACC	600
753	DB	AGGAGATGCAGGTATTGGTGTAGTGGATTGCAAGTTGGATGGCCACCCTACTCTGAATGACC	812
601	QY	ACTTAGAGCTTTGGATCCAGAGAAACGGCGCTGGGACATTTTGTGGATCTCTACGGGA	660
813	DB	ACTTAGAGCTTTGGATCCAGAGAAACGGCGCTGGGATATCTTTTGTGGAACTCTATGGGA	872
661	QY	ACAATGCAGACGCCAGAGAGCCGGAAGCCAGGAGCGTTTCAACCGCTGGTTCCTGACGG	720
873	DB	ACAATGCAGACGCCAGAGAGCCGGAAGCCAGGAAACGCTTCAACCGCTGGTTCCTGACGG	932
721	QY	GCATGACTGTGGCTGGTGTAGTTCTGTCTGGGCTCACTCTTTCAGTCGGAAGTGACCAGACA	780
933	DB	GCATGACTGTGGCGCGGTGGTTCTGTCTGGGCTCACTCTTTCAGTCGGAAGTGACAGACA	991
781	QY	CTGACCGTCCACTCACTCTCACTCCCACTGCCCGCCACCAAACTCTC	831
992	DB	CTGACCATCCACTTACCTCCACCCCTTCTCTGCTCCACACATCTCCGTC	1042

RESULT 11					
CK000319					
LOCUS		798 bp	mRNA	linear	EST 26-NOV-2003
DEFINITION	AGENCOURT 16368639	NIH MGC_220	Homo sapiens	cdna clone	
	IMAGE:30706817	5'	mRNA	sequence.	

Db 421 GGACAGCATATCAGAGCTTTGAACACAGGTAGTGAATGAATCTTCCGGGATGGGGTAAACT 480  
Qy 481 GGGGTGCGATGTGGCTTCTTCTCTTTGGGGGCACTGCTGGTGAAGAGCTAGACA 540  
Db 481 GGGGTGCGATGTGGCTTCTTCTCTTTGGGGGCACTGCTGGTGAAGAGCTAGACA 540  
Qy 541 AGGAGATCAGAGTATTGGTGTAGTGGATGCAAGTTGGATGGCCACCTTACCTGAATGACC 600  
Db 541 AGGAGATCAGAGTATTGGTGTAGTGGATGCAAGTTGGATGGCCACCTTACCTGAATGACC 600  
Qy 601 ACCTAGAGCTTTGGATCCAGAGAAACGGCGGTGGGAACCTTTTGTGTGATCTTACCGGA 660  
Db 601 ACCTAGAGCTTTGGATCCAGAGAAACGGCGGTGGGAACCTTTTGTGTGATCTTATGGGA 660  
Qy 661 ACATGACAGACCGAGAGCCGGAAGCCGAGGAGCTTTCAACGCTGGTTCTGTGAGG 720  
Db 661 ACATGACAGACCGAGAGCCGGAAGCCGAGGAGCTTTCAACGCTGGTTCTGTGAGG 720  
Qy 721 GCATGACTGTGGCTGTAGTCTTCTGTGGGCTCACTCTTCAGTGGGAAGTGACACAGACA 780  
Db 721 GCATGACTGTGGCGGGCTGGTCTGTCTGGGCTCACTCTTCAGTGGGAAGTGACACAGACA 780  
Qy 781 CTGACCGTCCACTC 794  
Db 781 CTGACATCCACTC 794

## RESULT 12

BQ924197  
LOCUS  
DEFINITION AGNCOURT\_886114 NIH\_MGC\_101 Homo sapiens cDNA clone IMAGE:6464133  
5', mRNA sequence.

ACCESSION BQ924197.1 GI:22339228

VERSION  
KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 922)

## REFERENCE

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: sgapbs-remail.nih.gov  
Tissue Procurement: ATCC

cDNA Library Preparation: Rubin Laboratory  
cDNA Sequencing Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLCM2656 row: 1 column: 22  
High quality sequence stop: 627.

## FEATURES

source

1. 922  
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/tissue\_type="epidermoid carcinoma, cell line"  
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/clone\_lib="NIH\_MGC\_101"  
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XhoI; cDNA made by oligo-dT priming. Directionally cloned  
into EcoRI/XhoI sites using the following 5' adaptor:  
GGCAGAG(G). Library constructed by Ling Hong in the  
Laboratory of Gerald M. Rubin (University of California,  
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and  
Superscript II RT (Life Technologies). Note: this is a  
NIH\_MGC Library."

## ORIGIN

BU053776 732 bp mRNA linear EST 26-AUG-2002  
LOCUS  
DEFINITION UI-M-PD0-bzf-b-13-0-UI.r1 NIH\_BMAP\_PD0 Mus musculus cDNA clone

Query Match 40.0%; Score 696.2; DB 5; Length 922;  
Best Local Similarity 85.6%; Pred. No. 2.2e-179;  
Matches 798; Conservative 0; Mismatches 123; Indels 11; Gaps 2;  
Qy 124 CCCAAGAAAGATACAGCTGGAGTCACTTTAGTCGATGTCGAAGAGAAACAGGACTGAAGCCC 183  
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Qy 184 CAGAGAAATCTGACACAGAAAGGAGACCCCACTGATGCATCAATGGAACCAATCCATCTCTGGC 243  
Db 61 CAGAAGGAGTGAATCGAGATGGAGACCCCACTGATGCATCAATGGAACCAATCTCTGGC 120  
Qy 244 ACCTGGCGGATAGCCCCGCGGTGAATCGAGTCACTGGCCACAGCAGCAGTGTGATGTCGC 303  
Db 121 ACCTGGCAGACAGCCCCGCGGTGAATCGAGTCACTGGCCACAGCAGCAGTGTGATGTCGC 180  
Qy 304 GGGAGGTAAATCCCATGGCAGCAGTGAAGCAAGCGCTGAGAGAGCGTGGCGATGAGTTTG 363  
Db 181 GGGAGGTGATCCCATGGCAGCAGTGAAGCAAGCGCTGAGAGAGCGTGGCGATGAGTTTG 240  
Qy 364 AACTGGCGGTACCGGAGAGCACTTCACTGATCTTAACATCCAGCTTCATATACCCCAAGGA 423  
Db 241 AACTGGCGGTACCGGCGGCACTTCACTGATCTTAACATCCAGCTTCATATACCCCAAGGA 300  
Qy 424 CAGCATATCAGAGCTTTGAACAGGTAGTGAATGAATCTTTTCGGGATGGGTAACCTGGG 483  
Db 301 CAGCATATCAGAGCTTTGAACAGGTAGTGAATGAATCTTTTCGGGATGGGTAACCTGGG 360  
Qy 484 GTCCATTTGTGGCTTCTTCTCTTTGGCGGGCACTGTGCGTGGAAAGCGTATAGCAAGG 543  
Db 361 GTCCATTTGTGGCTTCTTCTCTTTGGCGGGCACTGTGCGTGGAAAGCGTATAGCAAGG 420  
Qy 544 AGATGAGGTATTGGTCACTGCGATTCGAAAGTTGATGGCCACCTTCACTGATGACCAACC 603  
Db 421 AGATGAGGTATTGGTCACTGCGATTCGAAAGTTGATGGCCACCTTCACTGATGACCAACC 480  
Qy 604 TAGAGCTTGGATCCAGAGAAACGGCGGTGGGACACTTTTGTGATCTCTTACCGGAACA 663  
Db 481 TAGAGCTTGGATCCAGAGAAACGGCGGTGGGATCTTTTGTGAACTCTTATGGGAACA 540  
Qy 664 ATGACAGCGCGAGAGCCGGAAGGCGCAGGAGCGTTTCAACCGCTGGTTCTGACGGACA 723  
Db 541 ATGACAGCGCGAGAGCCGGAAGGCGCAGGAAACGCTTCAACCGCTGGTTCTGACGGACA 600  
Qy 724 TGACTGTGGTGTAGTCTGCTGGCTCACTCTTCACTGCGAAGTGACACGACACTG 783  
Db 601 TGACTGTGGTGTAGTCTGCTGGCTCACTCTTCACTGCGAAGTGACACGACACTG 660  
Qy 784 ACCGTCCACTCACCTCTCACCTCCACCTTGGCCCAACCAACTCTCTTTCAGCCACC 843  
Db 661 ACCATCCACTTACCTTCCACCTTCTCTGCTGACCATCCCTC-GTCCAGCCGCC 719  
Qy 844 ATTCTACCGAGAGAACCACTTACATGCAACTTCACGCCCTTCCCTTATATAGGGTTGGG 903  
Db 720 ATTGCCACCANGAAGCACTTACATGACGCCCATGCCCCACCTGCCCCATCAGCGGNTGGG 779  
Qy 904 CCTAGACGGAGTCCCTGCGAGTGTAGCTTTTAGAATCTACACGCTTCTGTGAAGCCAC 963  
Db 780 CCCAGATCTGGTCCCTTGCAGNCTAGTTTCTAGAAATTTATCACACTCTGTGTGAGA- ---- 834  
Qy 964 CTTCCCCCAACATCTCAGTTTCCCTTGGCCTCAAAACTCACAAGGTTTTTCTCTCAGATCAG 1023  
Db 835 -----CCCCACACCTCAGTTCCCTTGGGCTCAGAAATTTCCAAAATATCTGT 889  
Qy 1024 CTCCTTGGAGGCTGGCAGGAGTGGGAAGGGGT 1055  
Db 890 CCAAAGGAGGCTGGCCAGGAATGGGAAGGGTT 921

## RESULT 13

BU053776

LOCUS

DEFINITION







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Db      |||||GGATTGCAAGTTGGATGGCCACCTACCTGATGATGACCACTTAGAGCTTGGATCCAGGAGA 261
Qy      |||||ACGGCGGCTGGGACACTTTTGTGTGATCTCTACGGGAACAATGACAGCCGAGAGCCGGA 684
Db      |||||ACGGCGGCTGGGACACTTTTGTGTGATCTCTACGGGAACAATGACAGCCGAGAGCCGGA 321
Qy      |||||AAGCCACAGGAGCGTTTCAACCGCTGGTTCCTGACGGGCATGACTGTGGTGTAGTTC 744
Db      |||||AAGCCACAGGAGCGTTTCAACCGCTGGTTCCTGACGGGCATGACTGTGGTGTAGTTC 381
Qy      |||||TGCTGGGCTCACTCTTCAAGTCGGAAGTGACACAGACACTGACCGTCCACTCACCTCTCACC 804
Db      |||||TGCTGGGCTCACTCTTCAAGTCGGAAGTGACACAGACACTGACCGTCCACTCACCTCTCACC 441
Qy      |||||TCCCACCTTGGCCCCACACCAACTCTCTCTTTCAGCCACCATTTGCTACCAGGAGAACCACT 864
Db      |||||TCCCACCTTGGCCCCACACCAACTCTCTCTTTCAGCCACCATTTGCTACCAGGAGAACCACT 501
Qy      |||||ACATGCAACTCACGCCCCCTTCCCTTATATAGGGTTGGGCTTAGACGGAGTCCCTGCGAG 924
Db      |||||ACATGCAACTCACGCCCCCTTCCCTTATATAGGGTTGGGCTTAGACGGAGTCCCTGCGAG 561
Qy      |||||TTAGCTTTCTAGAACTACACGCTTCTGTGAAAGCCACCTTCCGCCCCACATCTCAGTTC 984
Db      |||||TTAGCTTTCTAGAACTACACGCTTCTGTGAAAGCCACCTTCCGCCCCACATCTCAGTTC 621
Qy      |||||CCTTGGGCTCAAACTCACAAAGTTTTCCTCAGATCAGCTCCTTGGAGGCTGGCAGGAG 1044
Db      |||||CCTTGGGCTCAAACTCACAAAGTTTTCCTCAGATCAGCTCCTTGGAGGCTGGCAGGAG 681
Qy      |||||TGGGAAGGGGTGTGCTAGAGGAGAGAGCCTGCTTGTGGTGGGACCTTGATTACCC 1103
Db      |||||TGGGAAGGGGTGTGCTANNAGGAGAGAGCTGCCCTTGT--GGTGGACCTTGATTACCC 738
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Search completed: March 31, 2005, 04:21:23  
Job time : 5252 secs

George Washington